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11-FEB-2000; 2000US-0181948
14-MAR-2000; 2000US-0189199
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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AAU99015
AAU99016
AAU99017
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AAB36897
                                                           AAB82673
AAB36894
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ALIGNMENTS

AAE08627 standard; Protein; 419 AA Human protein C derivative #1.

Human; protein C derivative, anticoagulation activity; thrombosis, serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.

Jones BE; Grinnell BW, Gerlitz BE,

Human protein C de

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11-FEB-2000; 2000US-0181948.
14-MAR-2000; 2000US-0189199.
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                                                 N-PSDB; AAD15226.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. mycardial infarction and unstable angina; and disease states predisposing to thrombosis, vascular occlusive disorders and hypercoagulable states e.g. thrombosis, vascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral haemorrhagic fever and hamman sickle cell disease, viral haemorrhagic fever and hamman anti-platelet agent; protein C deficiency; acute arterial trombotic cocclusion, thromboolism or stenosis in combination with a thrombolytic agent. Nucleic acid molecules of the invention are useful to for treating humans with genetically predisposed protein derivation are useful to the treating humans with genetically predisposed protein derivation of derivative for treating humans with genetically predisposed protein derivation are useful to the treating humans with genetically predisposed protein derivative for treating humans with genetically predisposed protein derivative for treating humans with genetically predisposed protein derivative for the der
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                                                                                                Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy. The present sequence is human protein C derivative
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14-MAR-2000; 2000US-0189199.
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                      WPI; 2001-514662/56.
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                                              N-PSDB; AAD15225
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Matches

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The Threation Feature to numein protein to derivatives have increased anticoagulation feature to melecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial information for the treatment of acute coronary syndromes e.g. myocardial informations; vascular occlusive dissease states predisposing to thrombosis; vascular occlusive dissorders and hypercoagulable states e.g. thalassaemia, sickle cell disease, viral hemorrhagic fever and permeability increasing protein; thrombotic disorders in combination with an anti-platelet agent; protein C deficiency; acute arterial permeability increasing protein; thrombotic disorders in combination with an anti-platelet agent; protein C deficiency; acute arterial or peripheral arteries or in vacular grafts in combination with a thrombolytic agent. Nucleic acid molecules of the invention are useful continuous to the contraction of the contraction of the continuous of the invention are useful thrombolytic dispreadents of the invention are useful the contraction of th
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91.0%; Score 182; DB 22
Best Local Similarity 79.5%; Pred. No. 1e-21;
Matches 35; Conservative 0; Mismatches
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2001-514662/56
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The present sequence is that of a claimed human protein C derivative in which Ser at amino acid position 11 of the mature wild-type protein C sequence (see AAB82673) is substituted with Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, and
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                                                                                                                                                                                                                            "cleavage makes a 2-chain inactive precursor (155-amino acid light chain attached via a disulfide bond to a
                                                                                                                                                                                                                                                                               262-amino acid heavy chain)"
"Leu in wild-type protein"
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14-MAR-2000; 2000US-0189197.
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                                                                     Disulfide-
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                  Domain
molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type bumen protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial infarction and unstable angina; and disease states predisposing to thrombosis; vascular occlusive disorders and hypercoagulable states e.g. disseminated intravascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral haemorrhagic fever and hemolytic uremic syndrome; sepsis in combination with bacterial thrombotic occlusion, thrombotic disorders in combination with an anti-platelet agent; protein C deficiency; acute arterial thrombotic occlusion, thromboemia grafts in combination with a trombotic occlusion, thromboemia grafts in combination with a tromboty agent. Nucleic acid molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders by gene therapy. The present sequence is human protein C derivative.
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                                                                                                                                                                                                                                            The invention relates to human protein C derivatives and nucleic acid
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                                                                                                                                    Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein C; human; coronary syndrome; thrombosis; angina; myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal; anticoagulant; therapy;
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                                                                                                                                                                                                          Claim 5; Page 48-49; 59pp; English.
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                                                  Jones
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                                                 Gerlitz BE, Grinnell BW,
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                (ELIL ) LILLY & CO ELI.
                                                                                 WPI; 2001-514662/56.
N-PSDB; AAD15227.
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Synthetic.
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            C derivatives of the invention that have at least 2 amino acid substitutions, but which have increased anticoagulant activity and resistantions, but which have increased anticoagulant activity and resistantion to inactivation by serpine compared with the wild-type protein, while retaining the biological activity of the wild-type protein. A method of producing the derivatives using recombinant combination or methods is claimed. The protein C derivatives are useful for treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina).

C vascular occlusive disorders and hypercoagulable states, sepsis (in combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders (in combination with an anti-platelet agent or by local delivery through thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral arterises or in vascular grafts. Human preference the such genetically predisposed prothrombotic disorders may
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 The protein is an example of protein
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                                                                                                                                                                                                                                                                                                                                                                Query Match 91.0%; Score 182; DB 22; Length 419; Best Local Similarity 79.5%; Pred. No. 1e-21; Matches 35; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein C derivative (S11G/Q32E/N33D/L194S/T254S)
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                                                                                                                                                                                                                                                                                                 be treated by gene therapy (all claimed).
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 position 194 with Ser.
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The present sequence is that of a claimed human protein C derivative in which Ser at position 11 of the mature wild-type protein C in which Ser at position 13 is substituted with Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, Leu at position 132 with Glu, Asn at position 254 with Ser. It is an example of protein C and Thr at position 254 with Ser. It is an example of protein C derivatives of the invention that have at least 2 amino acid canditions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild-type protein. A method of producing the derivatives using recombinant creating coronary syndromes and disease states predisposing to treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina). C vascular occlusive disorders and hypercoagulable states sepsis (in combination with an anti-platelet agent or by local delivery through
                                                                                                                                                                                                                                                                                                                   /note= "activation peptide; removal activates the 2-chain zymogen"
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            precursor (155-amino acid light chain attached via a disulfide bond to a 262-amino acid heavy chain)"
 "cleavage makes a 2-chain inactive
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/note= "N-glycosylated"
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14-MAR-2000; 2000US-0189197.
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/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
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  1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                        Modified GLA domain of vitamin K-dependent protein.
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                                                                                                                                  AAY18300 standard, peptide,
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                              therapy
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                                                                                                                    AAY18300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY18301
                                                                                             RESULT
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                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..44
/note= "Xaa= gamma-carboxyglutamic acid, or glutamic
acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary, ecrebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed).
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                                                                                                                                                                                 Length 419;
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                                                                                                                                                                                                                                                                                                        ANSFLEBLRHGSLERECIBBICDFEEAKBIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                     1 ANSFLXXLRHGSLXRXCIXXICDFXXAXXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain of vitamin K-dependent protein.
                                                                                                                                                                                                                           6
                                                                                                                                                                               91.0%; Score 182; DB 22;
79.5%; Pred. No. 1e-21;
iive 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 176; DB 20;
Pred. No. 8.9e-22;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY18297 standard; peptide; 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.0%;
97.7%;
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                                                                                                                                                                                                 Local Similarity 79.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
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                                                                                                                                       Sequence
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                                                     This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the affinity as compared to the native protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified GLA domain of vitamin K-dependent protein.
                                                                                                                                                                                                                                                                                                                                                                                                   Score 174; DB 20;
Pred. No. 1.9e-21;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY18301 standard; peptide; 44 AA
Claim 9; Page 79; 86pp; English.
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Best Local Similarity 97.7%;
Matches 43; Conservative
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Gaps

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1; Indels

1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

43; Conservative

Matches

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The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial infarction and unstable angina; and disease states predisposing to thrombosis, vascular occlusive disorders and hypercoagulable states e.g. thrombosis, vascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral hemorrhagic fever and permeability increasing protein; thrombolatic disorders in combination with an anti-platelet agent; protein C deficiency; acute arterial crimpobly in the arteries or in vascular grafts in combination with a thrombolytic agent, wholeic acid molecules of the invention are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for treating humans with genetically predisposed prothrombotic disorders by gene therapy. The present sequence is human protein C derivative.
                                                                                                                                                                                                                                                                                                                     Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein C; human; coronary syndrome; thrombosis; angina; myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal; anticoagulant; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 87.0%; Score 174; DB 22;
Best Local Similarity 77.3%; Pred. No. 2.2e-20;
Matches 34; Conservative 0; Mismatches 10
                                                                                                                                                                                                          Jones BE;
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                                          02-FEB-2001; 2001WO-US01221.
                                                                                     11-FEB-2000; 2000US-0181948.
14-MAR-2000; 2000US-0189199.
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 50-51; 59pp;
                                                                                                                                                                                                        Grinnell BW,
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N-PSDB; AAD15228.
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-OCT-2001
                                                                                                                                                                                                        Gerlitz BE,
16-AUG-2001
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ID AAB8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.
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                                                                                                                                                                                                   /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; protein C derivative, anticoagulation activity; thrombosis; serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                     GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANSFLXXLREGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE08630 standard; Protein; 419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 82; 86pp; English.
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                                                                                                                                                                                                                                                                                                                                                                98WO-US22152
                                                                                                                                                                                                                                                                                                                                                                                                             97US-0955636
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Matches 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 AA;
                                                                                                                                                                             Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nelsestuen GL;
                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                        WO9920767-A1
                                                                                                                                                                                                                                                                                                                                                                20-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-1997;
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                                                                                                                                                                                                                                                                                                                   29-APR-1999
                                                                                                               Synthetic
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22; Length 419; 10; Indels

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The present sequence is that of a claimed human protein C derivative in which His at position 10 of the mature wild-type protein C sequence (see AABS2673) is substituted with Glu, Ser at position 11 with Glu, Asn at position 13 with Asp, and Leu at position 32 with Glu, Asn at position 33 with Asp, and Leu at position 194 with Ser. It is an example of protein C derivatives of the invention that have at least 2 amino acid cubstitutions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild-type protein. While retaining the biological activity of the wild-type protein. A method of producing the derivatives using recombinant DNA methods is claimed. The protein C derivatives are useful for treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardmal infarction and unstable angina), combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitors), thrombotic disorders (in combination with an anti-platelet agent or by local delivery through thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts. Human parteries or in vascular grafts. Human parteries or in vascular grafts. Human parteries with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S/T254S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein C; human; coronary syndrome; thrombosis; angina; myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal; anticoagulant; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 419
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  arterial thrombotic occlusion, and thromboembolism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Gln in wild-type protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.0%; Score 174; DB 22;
77.3%; Pred. No. 2.2e-20;
ilve 0; Mismatches 10;
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/note= "Gla domain"
                                                         Claim 5; Page 54-55; 63pp; English
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Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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AAB82678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE LITE LITE LITE AND SOND THE STATE AND A STATE AND 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           removal activates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 precursor (155-amino acid light chain
attached via a disulfide bond to a
262-amino acid heavy chain)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "cleavage makes a 2-chain inactive
/note= "His in wild-type protein"
                                                      "Ser in wild-type protein"
                                                                                                                                                           note= "Asn in wild-type protein"
                                                                                                                                                                                                                     'note= "Leu in wild-type protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 158..169
| note= "activation peptide;
| 2-chain zymogen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "gamma-carboxylated"
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                                                                                                       note= "Gln in wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329
/note= "N-glycosylated"
                                                                                                                                                                                                                                                                           note= "Gla domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JAN-2001; 2001WO-US00020.
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14-MAR-2000; 2000US-0189197
                                                                                                                                                                                                                                                                                                                                                                                         .109
                                                      note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerlitz BE, Jones BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-496919/54.
                                                                                                                                                                                        Misc-difference 194
                                                                             Misc-difference 32
                            Misc-difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAH26365
                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
Disulfide-bond
Disulfide-bond
Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                        bond
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                                                                                                                                                                                                                                                                                                     Disulfide-h
Disulfide-h
                                                                                                                                                                                                                                                                                                                                                                                         Bulfide-
                                                                                                                                                                                                                                                                                                                                                                                                                                             sulfide-
                                                                                                                                                                                                                                                                                                                                                                                                                Bulfide
                                                                                                                                                                                                                                                                                                                                                            sulfide
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                                                                                                                                                                                                                                                 Domain
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Gaps

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protein. Amethod of producing the derivatives using recombinant DNA methods is claimed. The protein C derivatives are useful for treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina), vascular occlusive disorders and hypercoagulable states, sepsis (in combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders in an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral arterises or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed).
                                                                                                                                                                                                                    419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200270681-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB79950;
                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of a claimed human protein C derivative in which His at position 10 of the wild-type protein C sequence (see AAB82673) is substituted with Gln, Ser at position 11 with Gly, Gln at position 32 with Asp, Leu at position 194 with Ser, and Thr at position 254 with Ser. It is an example of protein C derivatives of the invention that have at least 2 amino acid substitutions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "activation peptide; removal activates the
2-chain zymogen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism -
                                                                                                                                             "cleavage makes a 2-chain inactive
precursor (155-amino acid light chain
attached via a disulfide bond to a
262-amino acid heavy chain)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "thrombin cleavage site"
                                                                                                                                                                                                                                               note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                           note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                      note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                   note= "gamma-carboxylated"
                                                                                                                                                                                                                    'note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                               note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                           note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                       note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "N-glycosylated"
329
/note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Page 56-57; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JAN-2001; 2001WO-US00020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-FEB-2000; 2000US-0179801
14-MAR-2000; 2000US-0189197
                                                                                                  331..345
                                                                                                                                                                                                                                                                                                                                                                                                                                     158..169
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                                                                                                                                                /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-496919/54.
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157193-A2
                                                                                                                                Cleavage-site
                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                  Modified-Bite
                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                       Adified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
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                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New variant blood coagulation component, useful for manufacturing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 medicament for treating or preventing coagulation disorders, e.g. thrombosis, comprises an anticoagulant activity in the protein C-anticoagulant system of blood .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the protein sequence of a mutated Gla
      Length 419;
                                                                                                                                                                                                                                               Protein C; Gla domain; human; blood clotting; anticoagulant;
thrombolytic; antiarteriosclerotic; cardiant; antiaggregant;
                                                                                                                                                                                                                                                                                                                                                                Ser"
                                                                                                                                                                                                                                                                                                                                                                                      'note= "wild-type Gln substituted by Glu"
                                                                                                                                                                                                                                                                                                                                                                                                               /note= "wild-type Asn substituted by Asp"
                             10; Indels
                                                                    1 ANSFLEBLINGSLERECIEBICDFEBAKEIFEDVDDILAFWSKH 44
                                                      1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                             note= "wild-type Asp substituted by
     Score 174; DB 22;
Pred. No. 2.2e-20;
                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TACT-) TAC THROMBOSIS & COAGULATION AB
                                                                                                                                                                                                                       Human protein C mutated Gla domain SED
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page -; 58pp; English
                                                                                                                                               ABB79950 standard; Protein; 45
     87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002; 2002WO-SE00363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-2001; 2001US-272466P
                                                                                                                                                                                              (first entry)
Query Match
Best Local Similarity 77.3'
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-713449/77.
                                                                                                                                                                                                                                                                                                                                       Key
Misc-difference 23
                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 32
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commain (N-terminal amino acids 1-45) of human protein C. The mutated Gla domain contains the substitution mutations D236, Q32E and N319L Protein C and activated protein C variants comprising a mutated Gla domain are provided by the invention. The variants comprising a contain at least 6, and optionally 7-10, amino acid substitutions. A preferred mutant (designated QGNSEDY, see ABB79946) has the mutations H100, S11G, S12N, D23S, Q32E, N33D and H44Y, and shows greatly enhanced anticosquiant activity in standard in vitro cosquiation assays. The present mutant (designated SED) was produced in an example from the invention as a step toward the produced on an example from the invention as a step toward the production of the QGNSEDY mutant Gla domain, and shows little, if any, improvement in anticosquiant activity over wild-type to production of the ORNSEDY mutant Gla domain, and shows little, if any, improvement in anticosquiant activity over wild-type the variants based on DNA technology, and with the use of the variants based on DNA technology, and with the use of the variants or APC resistance, or in diagnostic test systems for assaying components of the protein C-anticosquiant system (all attributed). The variants may also be used in treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..44
/note= "Xaa= gamma-carboxyglutamic acid, or glutamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                                                                                                                                                                                                                                                                                                                               intravascular coagulation.

Note: The present sequence is not shown in the specification but is derived from the human wild-type Gla domain sequence given on page 7 of the specification (see ABB79947).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 23; Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ANSFLEELRHSSLERECIEEICSFEEAKEIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified GLA domain of vitamin K-dependent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 170; DB 23;
Pred. No. 9.1e-21;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY18309 standard; peptide; 44 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Begt Local Similarity 75.0%;
Matches 33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             45 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nelsestuen GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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AAY18309
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                          This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the affinity as compared to the native protein.
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                        Score 168; DB 20; Length 44;
Pred. No. 1.9e-20;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                          1 ANSFLXXLRHSSLXRXCIXXICDFXXAFXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                      1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified GLA domain of vitamin K-dependent protein.
Disclosure; Page 79-80; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    AAY18299 standard; peptide; 44 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 78; 86pp; English.
                                                                                                                                                                                                          84.0%;
95.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                     Query Match
Best Local Similarity 95.5
Matches 42; Conservative
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                                                                                                                                                                            44 AA;
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                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy.
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                                                                    Gaps
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/note= "Xaa= gamma-carboxyglutamic acid, or glutamic
acid"
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                                                                       ö
      Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLA domain; vitamin K-dependent protein; clotting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 44;
                                                                    2; Indels
                                                                                                                                                                      ANSFLXXLRESSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                  1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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93.2%; Pred. No. 1.9e-20;
iive 2; Mismatches 1;
Score 168; DB 20;
Pred. No. 1.9e-20;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 14; 86pp; English
                                                                                                                                                                                                                                                                                                                                               AAY18303 standard; peptide; 44 AA.
         84.0%;
95.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein C GLA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
Query Match
Best Local Similarity 95.5
Matches 42; Conservative
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Best Local Similarity 93.2
Matches 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nelsestuen GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-OCT-1998;
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IID AAY18303

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Gaps

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1; Indels

ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFQNVDDTLAFWSKH 44

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Search completed: December 30, 2003, 09:18:18 Job time : 43 secs

1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

OM protein - protein search, using sw model

December 30, 2003, 09:16:41; Search time 21 Seconds (without alignments) 201.496 Million cell updates/sec Run on: .

US09497591-1EDITED

Perfect score:

1 ANSFLXXLRHGSLXRXCIXX.....XXAKXIFedVDDTLAFWSKH Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* **Database**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	protein C (activat	υ	protein C (activat	υ	coagulation factor	coagulation factor		coagulation factor	coagulation factor	U		coagulation factor	thrombin (EC 3.4.2	coagulation factor	plasma protein S p	plasma protein S p	coagulation factor	coagulation factor	plasma protein S -	plasma protein S p	plasma protein S p	ition facto	plasma protein S p	tion facto	thrombin (EC 3.4.2	plasma protein S p		plasma protein Z p	
SUMMARIES	KXHU	JX0210	S18994	KXBO	EXRT	EXBO	EXHU	146932	KPHU7	S10511	A35827	KFB07	TBHU	EXCH	S53434	KXHUS	A30351	JQ0419	S38819	KXBOS	KXRTS	KFHU	853433	KFBO	TBBO	KXMSS	KXBOZ	KXHUZ	A48089
DB	-	Н	н	-	н	-	н	~	-	~	~	-	-	~	~	н	-	~	~	-	н	-	~		-	-	-	-	7
Length	461	461	461	456	482	492	488	443	466	617	618	407	622	475	642	919	452	459	646	675	675	461	642	416	625	675	396	422	673
* Query Match	84.0	69.5	69.0	60.5	ė.	54.5	54.0	50.0	49.0	42.2	42.2	42.0	41.0	40.5	40.0	•	•	39.5	•	٥.	Θ.	۲.	è.	•	'n	34.5	۳.	31.8	30.0
Score	168	139	138	121	113	109	108	100	98	84.5	•	84	82	81	80	80	79	79	79	78	92	75	73	72	70	69	•	63.5	9
	-	7	ო	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23		25			28	29

growth potentiatin	growth arrest-spec	probable MAP kinas	probable MAP kinas	probable MAP kinas	hypothetical prote	hypothetical prote	alcohol dehydrogen	primosomal replica	protein-tyrosine k	hypothetical prote	hypothetical prote	ammonium transport	VSG expression sit	protein-tyrosine k	tyrosine kinase re
155476	B48089	D84859	C96575	G96763	T40556	T02367	S27994	G64062	158375	A83512	T25948	E82918	D32433	A48999	JC1189
7	~	~	N	N	~	~	-	7	7	~	~	7	~	~	7
674	678	594	603	576	909	1684	558	730	1363	1694	323	510	1235	1298	182
29.5	29.0	28.5	27.3	26.2	26.0	25.0	24.5	24.5	24.5	24.5	24.2	24.2	24.0	24.0	23.5
29	28	56.5	54.5	52.5	52	20	49	49	49	49	48.5	48.5	48	48	47
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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protein C (activated) (EC 3.4.21.69) precursor - human N.Alternate names: autoprothrombin IIA; plasma protein C C; Species: Homo sapiens (man) C; Bate: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999 C; Accession: A22331, A25426; A21781; A23789; A00927 R; Poster, D.C.; Yoshitake, S.; Davie, E.W. Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985 A; Title: The nucleotide sequence of the gene for human protein C. A; Reference number: A22331, MUID:85270390; PMID:2991887

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JY
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A/Introns: 2411; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
A/Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
A/Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
A/Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
C/Superfamily: coagulation effector X; EGF homology, GGLA>
C/Superfamily: coagulation beta-hydroxyaspartic acid; blood coagulation; calcium binding F;1-32/Domain: signal sequence #status predicted <SIG>
F;3-42/Domain: Gla domain homology <GGLA>
F;31-42/Domain: protein C light chain #status predicted <LCH>
F;31-13/Domain: EGF homology <CGL>
F;41-197/Product: protein C light chain #status predicted <LCH>
F;20-461/Product: protein C heavy chain #status predicted <HCH>
F;20-461/Product: protein C heavy chain #status experimental <APT>
F;21-445/Domain: activation peptide #status experimental <APT>
F;21-445/Domain: activation peptide #status experimental <APT>
F;21-445/Domain: activation peptide #status gamma-carboxyglutamic acid (Glu) #status experimental <APT>
F;21-445/Domain: activation peptide #status predicted (Asp) #status experimental <APT>
F;21-445/Domain: activation peptide #status acid (Asp) #status experimental <APT-
F;31-445/Domain: activation peptide #status predicted (Asp) #status experimental <APT-
F;31-445/Domain: activation #status experimental <APT-
F;31-22/Claavage site: arbohydrate (Asp) (covalent) #status experimental <APT-
F;113/Additied site: carbohydrate (Asp) Ser #status predicted (F:253,299,402/Active site: His, Asp, Ser #status predicted (F:253,299,402/Active site: Rexperimental (Asp) (Astatus predicted (Asp) (Astatus atypical (Asp)) (Asylanding site: carbohydrate (Asp) (covalent) (Asputial) #status atypical
C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKH 86
                                                                                                                                                                                                              A; Cross-references: GDB:120317; OMIM:176860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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A,Gene: GDB:PROC
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A; Molecule type: mRNA
A; Residues: 1-461 < COKA2.
A; Molecule type: mRNA
A; Residues: 1-461 < COKA2.
A; Cross-references: EMBL: X64336; NID: 956962; PIDN: CAA45617.1; PID: 956963
A; Cross-references: EMBL: X64336; NID: 956962; PIDN: CAA45617.1; PID: 956963
C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; Lrypsin homology
C; Keywords: beta-hydroxyapartic acid; glycoprotein; hydrolase; serine proteinase
F; 1-32 Domain: signal sequence #status predicted < SIG>
F; 27-85 Domain: BGF homology < CIG>
F; 33-42 Domain: propeptide #status predicted < PRC>
F; 31-340 Domain: EGF homology < CIG>
F; 1-130 Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F; 121-130, 139-150, 146-159, 161-174, 182-320, 239-355, 373-387, 398-426/Disulfide bonds: #statu
F; 211-130, 139-150, 146-159, 161-174, 182-320, 239-255, 373-387, 398-426/Disulfide bonds: #statu
F; 215, 291, 355/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 254, 300, 402/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                protein C (activated) (EC 3.4.21.69) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Accession: 518994; S24312
R;Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
submitted to the RMBL Data Library, Pebruary 1992
A;Description: The CDNA cloninig and mRNA expression of rat protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Directin C (activated) (EC 3.4.21.69) precursor - bovine (fragment)
NyAlternate names: autoprothrombin IIA; plasma protein C
C;Species: Bos primiganius taurus (cattle)
C;Date: 30-Nov-1980 #sequence_revision II-Mar-1987 #text_change 16-Jul-1999
C;Accession: A26250; A18385; A18386; A00928
R;Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5633-5656; 1984
A;Title: Cloning and sequence of liver cDNA coding for bovine protein C.
A;Reference number: A26250; MUID:85014826; PMID:6091100
                                                                                      Gaps
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Kesidues: 1-461 - COKA>
A;Cross-references: ENBL:X64336; NID:956962; PIDN:CAA45617.1; PID:956963
R;Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
B;Ochiu, Biophya. Acta 1131, 329-332, 1992
A;Title: The CDNA cloning am RNA expression of rat protein C.
A;Reference number: S24312; MUID:92329550; PMID:1627650
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Length 461;
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Best Local Similarity 59.1%; Pred. No. 3e-14;
Matches 26; Conservative 7; Mismatches 11; Indels
                                                                              11; Indels
                                                                                                                                                                                                     1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
Query Match
69.5%; Score 139; DB 1;
Best Local Similarity 59.1%; Pred. No. 2e-14;
Matches 26; Conservative 7; Mismatches 1
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A;Residues: 1-456 <LON>
R;Fernlund, P.; Stenflo, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: S24312; Status: preliminary
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A; Note: submitted to the EMBL Data Library, June 1994
A; Note: neither the complete nucleic acid sequence nor the complete translation are shown R; Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 189, 269-273, 1996
A; Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A; Reference number: JC4670; MUID:96194815; PMID:8647460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ',Residues: 1-482 <STA2>

',Cross-references: BMBL.X79807, NID:g506600, PIDN:CAA56202.1; PID:g506601

',Experimental source: Cos-1 cell

',Enjyoji, K.; Miyazaki, K.; Kato, H.

Blacchem. 109, 890-898, 1991

',Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plast

',Title: Characterization of mUID:92041742; PMID:1718949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    i.Pathway: blood coagulation
Suberfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology;
Subperfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology;
Subperfamily: perpentic acid; blood coagulation; calcium binding; carboxyglutamn;
1-23/Domain: signal sequence #status predicted <PRO>
1-24-40/Domain: gla domain homology <GLA>
1-25-84/Domain: Gla domain factor X light chain #status predicted <LCH>
1-11/Domain: EGF homology <EGI>
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F;46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #statu
F;46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #statu
F;57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,41:
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;108/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;208/Binding site: carbohydrate (Asn) (covalent) #status predicted
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F;274,320,417/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
M;Molecule type: Bottein
R;Mesidues: 183-186, X'.188-207, cENJ2>
R;Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Bur. J. Haematol. 52, 162-168, 1994
A;Title: Analysis of the partial nucleotide sequences and deduced primary structures of A;Reference number: 146196; MUID:94222160; PMID:8168596
A;Accession: 162745
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F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
F:183-231/Domain: activation peptide #status predicted <APT>
F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
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NiAlternate names: Stuart factor
C.Species: Bos primigenius taurus (cattle)
C.Species: 24-Apr-1984 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
                                                                                               Residues: 1-482 <STA1>
;Cross-references: EMBL:X79807; NID:g506600; PIDN:CAA56202.1; PID:g506601
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;Molecule type: DNA
;Residues: 255-383, 'G', 385-455 cMUR>
;Cossiques: 256-383, 'G', 385-455 cMUR>
;Coss-references: GB:D21215; NID:9415309; PIDN:BAA04756.1; PID:9455396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: protein;Residues: 41-58,'X',60-65 <ENJ1>;Accession: PS0190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: JC4670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: PS0191
     A;Accession: S49075
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C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin C;Guperfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology C;Keyvords: anticoagulant; beta-hydroxysspartic acid; blood coagulation; calcium binding F;1-29/Domain: signal sequence (fragment) #status predicted <SIG>
F;20-39/Domain: signal sequence (fragment) #status predicted <SIG>
F;30-39/Domain: gla domain homology <GLA>
F;30-194/Product: protein C light chain #status experimental <LCH>
F;30-194/Product: protein C light chain #status experimental <ACH>
F;30-194/Product: protein C heavy chain #status experimental <ACH>
F;30-195/Domain: activation peptide #status experimental <ACH>
F;30-195/Product: protein C heavy chain #status experimental <ARP>
F;30-146/Domain: activation peptide #status experimental <ARP>
F;30-146/Domain: activation peptide #status experimental <ARP>
F;31-148/DMOdified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental F;110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted F;110/Modified site: carbohydrate (Asm) (covalent) #status predicted F;252,298,397/Active site: His, Asp, Ser #status predicted F;256/Blinding site: carbohydrate (Asm) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 197.454, PV .cSTE>
A;Residues: 197.454, PV .cSTE>
B;Resmon, N.L.; DeBault, L.B.; Esmon, C.T.
J. Biol. Chem. 258, 5548-5553, 1983
A;Title: Protecolytic formation and properties of gamma-carboxyglutamic acid-domainless parefracence number: A37541; MUID:83213513; PMID:6304092
A;Contentes: annotation; activation; alcium binding
B;Johnson, A.E.; Esmon, N.L.; Laue, T.M.; Esmon, C.T.
J. Biol. Chem. 258, 5554-5560, 1983
A;Title: Structural changes required for activation of protein C are induced by Ca2+ bir A;Reference number: A37542; MUID:83213514; PMID:6406503
A;Contents: annotation; activation; calcium binding
C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
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A;Reference number: A58498; MUID:96093366; PMID:8578539
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coagulation factor Xa (EC 3.4.21.6) precursor - rat
coagulation factor Xa (EC 3.4.21.6) precursor - rat
C;Species: Rattus norvegicus (Norvey rat)
C;Species: 31-dan-1995 #sequence revision 07-Reb-1997 #text_change 08-Dec-2000
C;Accession: S49075; JC4670; PS0191; PS0190; I62745
R;Stanton, C.; Rose, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
A;Title: Evidence for competition between vitamin K-dependent clotting factor
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Ajmolecule type: protein
Ajmolecule type: protein
Ajmolecule type: 4cpRx-
Ajnote: 82-Ly8 was also found
Ajnote: 82-Ly8 was also found
Proc. Natl Acad. Sci. U.S.A. 80, 1802-1806, 1983
Ajritle: beta-Hydroxysaparitc acid in vitamin K-dependent protein C.
Ajritle: beta-Hydroxysaparitc acid in vitamin K-dependent protein C.
Ajritle: annotation; revision to residue 110
Rjstenflo, J.; Fernlund, P.
J. Biol. Chem. 257, 12180-12190, 1982
Ajritle: Amino acid sequence of the heavy chain of bovine protein C.
Ajritle: Amino acid sequence of the heavy chain of bovine protein C.
Ajreference number: Al8386; MUID:83007326; PMID:6896877
                              A; Title: Amino acid sequence of the light chain of bovine protein C. A;Reference number: A18385; MUID:83007325; PMID:6896876 A;Accession: A18385
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Pred. No. 1.6e-11;
9; Mismatches 12; Indels
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Matches 21; Conservative
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F;57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status pr F;57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status pr F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental F;200/Binding site: sulfate (Tyr) (covalent) #status experimental F;218,481nding site: carbohydrate (Thr) (covalent) #status experimental F;218/Binding site: carbohydrate (Asn) (covalent) #status experimental F;218/Binding site: Carbohydrate (Asn) (covalent) #status experimental F;218/Binding site: Arg-1le (coagulation factor IXa, coagulation factor VIIa) #statu F;240-245,260-276,389-403,414-442/Disulfide bonds: #status experimental
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Cibace: 15-Nov-1994 #sequence revision 02-May-1994 #text_change 08-Dec-2000
Cibaces is-Nov-1994 #sequence revision 02-May-1994 #text_change 08-Dec-2000
Cibacession: A24478; JG0917; A42485; A25853; A22208; A21284; A20362; S39415; I54051; A009: R;Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, B.W.
Blochemistry 25, 5098-5102, 1986
A;Fitle: Gene for human Factor X: a blood coagulation factor whose gene organization is & A;Reference number: A24478; MUID:87026600; PMID:3768336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Accession: A24478
A; Molecule type: DNA
A; Cross-references: GB: M14327; NID: 9459809; PIDN: AAA52764.1; PID: 9182831
R; Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
Gene 99, 291-294, 1991
A; Mille: Cloring and expression in COS-1 cells of a full-length cDNA encoding human coagn
A; Reference number: JQ0917; MUID: 91216473; PMID: 1902434
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A, Residues: 1-488 < MES>
A; Cross-references: GB MS7285; NID:g182389; PIDN:AAA52421.1; PID:g182390
R; Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
J. Biol. Chem. 267, 7335-7401, 1992
A; Title: Liver-specific expression of the gene coding for human factor X, a blood coagul?
A; Reference number: A42485; MUID:92218390; PMID:11313796
                                                                                the proteolytic activation of prothrombin to thrombin in the pre
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A;Title: Isolation and characterization of human blood-coagulation factor X cDNA.
A;Reference number: A25853; MUID:86221713; PMID:3011603
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Pred, No. 1.5e-09;
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A; Residues: 19-284, 'E', 289-488 <KAU>
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Best Local Similarity 43.2
Matches 19; Conservative
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A; Residues: 1-15 <MIA>
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A/Recession: B5-126 c-PER.

A/Recession: B5-126 c-PER.

A/Recession: B39414

A/Recession: B49414

A/Recession: B49414

A/Recession: B49414

A/Recession: A11444

A/Recession: A11
C; Accession: A22867; A14997; A12030; A34412; S33414; A00925
R; Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.
Nucleic Acids Res. 12, 4481-4492, 1984
A; Title: Blood coagulation factor x mRNA encodes a single polypeptide chain containing a A; Reference number: A22867; MUID: 84247315; PMID: 6330671
A; Mccession: A22867; MUID: 84247315; PMID: 6330671
A; Mcserences: Tellos MRNA
A; Residues: 1-487 cFUN>
A; Cross-references: GB: X06673; NID: 9192; PIDN: CAA25286.1; PID: 9193
A; Cross-references: GB: X0673; NID: 9192; PIDN: CAA25286.1; PID: 9193
A; R: Enfield, D.L.; Ericson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
Biochemistry 19, 659-667, 1980
A; Title: Anino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
A; Mcference number: A14997; MUID: 80130563; PMID: 6766735
A; Mclecule type: protein
A; Residues: 41-102, 'N', 104-180 cENF>
A; McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A; Reference number: A20274; MUID: 83308813; PMID: 6688526
A; Contents: annotation; revision to residue 103
A; Reference number: A20274; MUID: 83308113; PMID: 668856
A; Contents: annotation; revision to residue 103
A; Reference number: A20374; MUID: 8308206, 1978
A; Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
A; Reference number: A12030; MUID: 76053069; PMID: 1059093
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W;Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
W;Sugo, T.; Bjork, I.; Holmgren, S.
W;Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic
A;Reference number: A38024; MUID:84185716; PMID:6546930
A;Contents: annotation; calcium binding
B;Morita, T.; Jackson, C.M.
J; Biol. Chem. 261, 4008-4014, 1986
A;Reference number: A38025; MUID:86140210; PMID:3949800
A;Contents: annotation; sulfate binding
C;Comment: Factor Xa converts prothrompin to thrombin during blood clotting.
C;Comment: The two chains are formed from a single-chain precursor by the excision of tw
C;Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), c
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A;Gene: F10
A;Map position: 13q34
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A,Molecule type: protein
A,Rebidues: 183-292,294-295, 'GDE', 299-334,336-348,'AE',351-354,356-441,'GKFG',446-492 <1
A,Note: carbohydrate binding sites and disulfide bonds were determined
R,Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
Baol. Chem. 264, 16897-16904, 1989
A,Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
A,Reference number: A34412; MUID:89380326; PMID:2789221
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A; Accession: A12030

activation.

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Gaps .. 0

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Coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Spacession: A28322; A23819; A31186; B31186; S63524
R;O'Hara, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murrie Proc. Natl. Acad. Sci. US.A. 84, S158-S162, 1987
A;Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depende A;Reference number: A28322; MUID:87260948; PMID:3037537
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;Cross-references: GB:M13232; NID:g182799; PIDN:AAA88040.1; PID:g182801
;Thim, L.; Bjoern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.F
iochemistry 27, 7785-7793, 1988
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    F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental 1:199,211/Binding site: carbohydrate (Thr) (covalent) #status experimental F;221,231/Binding site: carbohydrate (Asn) (covalent) #status experimental F;234,235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #statu F;276,322,419/Active site: His, Asp, Ser #status experimental
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Cispecies: Oryctolagus cuniculus (domestic rabbit)
Cjate: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
CjAccession: 146932
RiBrothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Alromb. Res. 69, 231-238, 1993
AjTitle: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-443 cBRO>
A;Cross-references: GB:S56300; NID:g266294; PID:g266295
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trýpsin homology
F;24-83/Domain: Gla domain homology <GLA>
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A;Molecule type: DNA
A;Residues: 1-466 -COHA>
A;Cross-references: GB:J02933; NID:g180333; PIDN:AAA51983.1; PID:g180334
A;Cross-references: GB:J02933; NID:g180333; PIDN:AAA51983.1; PID:g180334
B;Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, Proc. Natl. Acadé. Sci. U.S.A. 83, 2412-2416, 1986
A;Title: Characterization of a cDNA coding for human factor VII.
A;Reference number: A23819; MUID:86205965; PMID:3486420
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Pred. No. 2.2e-09;
8; Mismatches 17; Indels
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ive 5; Mismatches 17.
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                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 43.2%;
Matches 19; Conservative 8
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nes 19; Conservative
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Matches
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A; Residues: 1-23 - RES>
A; Crose-references: GB: M33297; NID:g183860; PIDN:AAA52636.1; PID:g553330
B; Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bla
A; Mol. Biol. 232, 947-966, 1993
A; Title: Structure of human dest[1-45] factor X at 2.2 angstroms resolution.
A; Reference number: A49458; MUID:93360277; PMID:8355279
A; Contents: annotation; X-ray crystallography, 2.2 angstroms
C; Comment: The two chains held together by one disulfide bond are formed from a single-C; Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fi129-164/Domain: Edr homology <EG2>
Fi183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
Fi183-488/Product: coagulation factor X heavy chain #status experimental <APT>
Fi183-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
Fi183-462/Domain: trypsin homology <TRY>
Fi235-462/Domain: trypsin homology <TRY>
Fi46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat
Fi57-62/Disulfide bonds: #status predicted
Fi90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: mRNA; Residues: 13.284, E', 289-488 <LB2>; Residues: 13.284, E', 289-488 <LB2>; Residues: 13.284, E', 289-488 <LB2>; Cross-references CB:KO1886; M. K.; Kisiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weins iochemistry 22, 2875-2884, 1983; M. K.; Kisiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weins iochemistry 22, 2875-2884, 1983; M. Kisiel, M. K.; Kisiel, M. K.; Kisiel, W.; Kwa, E.Y.; Weins iochemistry 22, 2875-2884, 1983; M. Kisiel, M.; Kwa, E.Y.; Weins in the complete amino acid sequence of the light chain of human blood coagulation fact is reference number: A20362; MUID:83257207; PMID:6871167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ਚ
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                                                                                                                                         coding for human blood coagulati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 183-234 < 1NO>
A; Note: 1917cosylation sites
A; Note: identification and characterization of beta-hydroxyaspartic acid
B; Jaqadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhushanam, K.; Lyman, G.
Game 84, 517-519, 1989
A; Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
A; Reference number: 154051; MUID:90128299; PMID:2612918
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F;24-40/Domain: signal sequence #status prediction.

F;25-84/Domain: gla december of status prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: protein
;Mealdues: 41-179 <MCM>
;Inoue, K.; Morita, T.
ur. J. Biochem. 218, 153-163, 1993
;Title: Identification of O-linked oligosaccharide chains in the activation peptides (;Title: Identification of O-linked oligosaccharide chains in the activation peptides (;Reference number: S39414; MUID:94062825; PMID:8243461
;Cross-references: GB:M22613; NID:g180335; PIDN:AAA51984.1; PID:g180336; Pung, M.R.; Hay, C.W.; MacGillivray, R.T.A. roc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985 roc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985 roc. Characterization of an almost full-length cDNA coding for human; Reference number: A22208; MUID:85216545; PMID:2582420
                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 13-441,'S', 443-488 <FUN>
A; Residues: 13-441,'S', 443-488 <FUN>
A; Cross-references: GB: K03194; NID: g182840; PIDN: AAA52490.1; PID: g182841
R; Leytus, S.P.; Chung, D.W.; Kisiel, W.; Kurachi, K.; Davie, E.W.
R; Leytus, S.P.; Chung, D.W.; Xisiel, W.; Kurachi, K.; Davie, E.W.
A; Title: Characterization of a cDNA coding for human factor X.
A; Reference number: A21284; MUID: 84222026; PMID: 6587384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: translation not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A20362
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42.2%; Score 84.5; DB 2; Length 618;
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AyAccession: 13634-13634
AyAccession: 13634-13634
AyAccession: 13634-13634
AyAccession: 13634-13634
AyAccession: 1364-13634
AyAccession: 1364-13634
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AyAccession: 1364-13634
AyAccession: 1364-1364-1364
AyAccession: 1364-1364
AyAccession: 1364-1364-1364
AyAccession: 1364-1364
AyAAccession: 1364-136
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S.10511

through (EC 3.4.21.5) precursor - rat

C.Species: Rattus norvegicus (Norway rat)

C.Species: Rattus norvegicus (Norway rat)

C.Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 03-May-2002

C.Accession: $10511, A60576; B42696

R.Dihanich, M.; Monard, D.

Nucleic Acids Res. 18, 4251, 1990

A.Title: cDNA sequence of rat prothrombin.

A.Accession: $10511, MUID: 90332426; PMID: 2377469

A.Accession: $10511

A.Molecule type: mRNA

A.Accession: $10511

A.Accession: $
A;Residues: 61-212 <THI>
A,Accession: B31186
A;Accession: B31186
A;Accession: B31186
A;Accession: B31186
A;Accession: B31186
A;Accession: Chem. 213-466 <TH2>
R;Bjoern, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Peder J. Biol. Chem. 266, 11051-11057, 1991
A;Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a A;Reference number: A40529; MUID:91250411; PMID:1904059
A;Contents: annotation; carbohydrate binding sites
A;Contents: annotation; carbohydrate binding sites
A;Contents: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox
A;Reference number: S63524; MUID:96096752; PMID:8529655
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Les 20; Conservative
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A;Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat uter R;Banfield, D.K.; MacGlllivray, R.T.A.
R;Banfield, D.K.; MacGlllivray, R.T.A.
Proco. Natl. Acad. Sci. U.S.A. 89, 2779-7783, 1992
Proco. Natl. Acad. Sci. U.S.A. 89, 2779-7783, 1992
Proco. Natl. Acad. Sci. U.S.A. 89, 2779-7783, 1992
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seqn. A;Reference number: A42696, MUID:92212913; PMID:1557383
A;Accession: B42696
A;Actus: preliminary
A;Molecule type: mRNA
A;Residues: 383-617, E' <BAN>
A;Cross-references: GB:M81397
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C;Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydromain: signal sequence #status predicted <SIG>F;1-24/Domain: signal sequence #status predicted <SIG>F;2-43/Domain: Gla domain homology <GLA>
F;28-88/Domain: Gla domain homology <GLA>
F;28-88/Domain Homology <GLA>
F;28-88/Domain Gla doma
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F;109-187/Domain: kringle homology <RR1>
F;215-292/Domain: kringle homology <RR2>
F;215-292/Domain: trypsin homology <RR2>
F;50.51-59,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F;61-66,91-104,109-187,130-170,1S8-182,215-292,236-276,264-287,332-478,387-403,532-546,5f F;402,458,564/Active site: His, Asp, Ser #status predicted
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A;Molecule type: mRNA
A;Residues: 1-618 cDEG
A;Residues: 1-618 cDEG
A;Residues: 1-618 cDEG
A;Cross-references: GB:X52308; NID:g53813; PIDN:CAA36548.1; PID:g53814
A;Experimental source: strain C57BL/6
A;Note: the data ware obtained from females resulting from the cross of M. domesticus and R;Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A;Titla: Partial characterization of vertebrate prothrombin cDNAs: amplification and seqn. A;Reference number: A42696; MUID:92212913; PMID:1557383
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 384-618, 'E' < sAN>
C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C; Reywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydrc
F; 25-43/Domain: gropeptide #status predicted < SAN>
F; 28-88/Domain: Gla domain homology < GLA>
F; 28-88/Domain: kringle homology < RR2>
F; 361-610/Domain: kringle homology < RR2>
F; 361-610/Domain: trypsin homology < RR2>
F; 361-66, 91-104, 109-187, 130-170, 158-182, 215-233, 236-276, 264-288, 333-479, 388-404, 533-547, 56
F; 403, 459, 565/Active site: His, Asp, Ser #status predicted
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Best Local Similarity 42.2%; Pred. No. 1.8e-05;
Matches 19; Conservative 5; Mismatches 20; Indels
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A; Molecule type: protein
A; Residues: 315-334, Nr, 336-348, Nr, 350-368, Nr, 370-397, Nr, 399-413, Nr, 415-484, Nr, 486-4
R; Residues: 315-334, Nr, 336-348, Nr, 350-368, Nr, 370-397, Nr, 399-413, Nr, 415-484, Nr, 486-4
R; Residues: 315-334, Nr, 186-13215, 1986
A; Reference number: A37551; MUID: 87008532; PMID: 3759958
A; Contents: annotation; activation cleavages
R; Macdillivray, Rr.; Irwin, D.M.; Guinto, E.R.; Stone, J.C.
R; Macdillivray, Rr.; Irwin, D.M.; Guinto, E.R.; Stone, J.C.
A; Richer Recombinant genetic approaches to functional mapping of thrombin.
A; Reference number: IS1952; MUID: 87182874; PMID: 3471151
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A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Residues: 1.2, RI',5-100 <RES.
A;Residues: 1.2, RI',5-100 <RES.
A;Residues: 1.2, RI',5-100 <RES.
A;Croment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrir C;Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds or an be removed either by factor Xa or thrombin; the cleavage into light and heavy chair ter 314-Arg, are released in natural blood clotting.
C;Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma. C;Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxyl ent interaction with the negatively charged phospholipid membrane surface.
C;Comment: The prothrombin precursor is synthesized in the liver.
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(Introns: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552/1; Introns: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552/1; Superfamily: thrombin; Gla domain homology, kringle homology; trypsin homology; Krywords acute phase; blood coagulation; calcium binding; carboxyglutamic acid; duplic file. 24/Domain: signal sequence #status predicted <SIG>7:1-24/Domain: signal sequence #status predicted <PRO>7:25-43/Domain: Gla domain homology <GLA>7:28-87/Domain: Gla domain homology <GLA>7:28-87/Domain: Gla domain homology <CLA>7:28-87/Domain: Gla domain homology <CLA>7:28-87/Domain homology <CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 44-118,'N',120,'S',122-163,'I',165-175,'A',177-182,'T',184-193,'MV',196-308,'
Bibutkowski, R.J.; Blion, J.; Downing, M.R.; Mann, K.G.
J. Biol. Chem. 252, 4942-4957, 1977
A;Title: Primary structure of human prethrombin 2 and alpha-thrombin.
A;Reference number: A37550; MUID:77207112; PMID:873923
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F;49,50,57,59,62,63,68,68,69,72,75,70,Modified site: gamma-carboxyglutamic acid (Glu) #status
F;60-65,90-103,108-186,129-169,157-181,213-291,234-274,262-286/Disulfide bonds: #status
F;121,143/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-622 < DBG>
A; Residues: 1-622 < DBG>
A; Residues: 1-622 < DBG>
A; Cross-references: GB:M31691; NID:g558069; PIDN:AAC63054.1; PID:g339641
R; Degen, S.J.F.; MacGillivray, R.T.A.; Davie, E.W.
Biochemistry 22, 2087-2097, 1983
A; Title: Characterization of the complementary deoxyribonucleic acid and gene coding
A; Reference number: A00914; MUID:83231469; PMID:6305407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A00914
A;Molccule type: mm.
A;Residues: 8-163, N',165-622 <DE2>
A;Residues: 8-163, N',165-625 <B3-J00307; NID:937128; PIDN:CAA23842.1; PID:91335344
A;Cross-references: GB:V00595; GB:J00307; NID:937128; PIDN:CAA23842.1; PID:91335344
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;213-291/Domain: kringle homology «KR2»
;238-361/Product: thrombin light chain #status experimental «LCH»
;364-622/Product: thrombin heavy chain #status experimental «HCH»
                                            Biochemistry 26, 6165-6177, 1987
A;Title: Nucleotide sequence of the gene for human prothrombin.
A;Reference number: A29351; MUID:88077877; PMID:2825773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;44-622/Product: prothrombin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: B00914
A;Molecule type: DNA
A;Residues: 188-311 <DE3>
R;Walz. D.A.; Hewett-Emmett, D.; Seegers, W.H.
Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977
A;Reference number: A37549; MUID:77193964; PMID:266717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: A37550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coagulation factor VIIa (EC 3.4.21.21) - bovine
coagulation factor VIIa (EC 3.4.21.21) - bovine
C;Species: Bos primigentus taurus (cat1e)
C;Species: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999
C;Accession: A31979; C20274
R;Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.
J. Biol. Chem. 263, 14868-14877, 1988
A;Title: Bovine factor VII. Its purification and complete amino acid sequence.
A;Recience number: A31979; MUID:89008362; PMID:3049594
A;Molecule type: protein
A;Residues: 1-407 ATAk>
R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A;Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood cc
A;Reference number: A20274; MUID:83308813; PMID:6688526
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A;Regidues: S8-62, X', 64-68 «MCM»
A;Nore: the residue designated 'X' was determined to be hydroxyaspartic acid
R;Hage, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,
J. Biochem. 104, 867-868, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombin (EC 3.4.21.5) precursor [validated] - human N.Alternate names: coagulation factor II N.Contains: prothrombin C.Species: Hono sapiens (man) C.Species: Hono sapiens (man) C.Species: Hono sapiens (man) C.Species: Hono: 30-Nov-1980 #sequence revision 22-Jul-1994 #text change 08-Dec-2000 C.Accession: A29351; A00914; B00914; A37549; A37550; I51952
                                                      Gaps
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Pred. No. 1.4e-05;
                                                                                                                                                                                                       44 ANSGFLEELRKGNLERECVEEQCSYEEAFEALESPQDTDVFWAKY 88
Pred. No. 1.8e-05;
5; Mismatches 20; Indels
                                                                                                                                                1 ANS-FLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Indels
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                                                 5; Mismatches
42.2%;
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Best Local Similarity 43.9%;
Matches 18; Conservative
                                            19; Conservative
Best Local Similarity
Matches 19; Conserv
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RESULT 13

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C;Accession: S53434
R;Greengard, J.S.; Pernandez, J.A.; Radtke, K.P.; Griffin, J.H.
Biochem. J. 305, 397-403, 1395
A;Title: Identification of candidate residues for interaction of protein S with C4b binds
A;Reference number: S53433, MUID:95134217; PMID:7832752
A;Accession: S53434
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat homory. Superfamily: plasma protein S; EGF homology; GLA>
F;1-51/Domain: signal sequence (fragment) #status predicted <SIG>
F;8-642/Product: plasma protein S #status predicted <MAT>
F;8-7-120/Domain: EGF homology <EG1>
F;87-120/Domain: EGF homology <EG3>
F;177-165/Domain: EGF homology <EG3>
F;217-207/Domain: EGF homology <EG4>
F;213-248/Domain: EGF homology <EG4>
F;21
                                                         C;Species: Macaca mulatta (rhesus macaque)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 16-Jul-1999.
     precursor, vitamin K dependent - rhesus macaque (fragment) a mulatta (rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 ANSMLETTKOGNLERECIEELCNKEEAREVFENDPETDYFYPKY 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Experimental source: tissue type liver A, Note: the source is designated as rhesus monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;291-444/Domain: laminin G repeat homology < LGR>
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Best Local Similarity 36.4%
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-642 <GRE>
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C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C; Superfamily: coagulation factor X; EGF homology; Gla domain superfamily: coagulation factor X; EGF homology; Gla domain; aginal sequence #status predicted <SIG>
F; 1-20/Domain: propeptide #status predicted <PRO>
F; 21-40/Domain: propeptide #status predicted <PRO>
F; 28-40/Domain: Gla domain homology <GLA>
F; 41-185/Product: coagulation factor X light chain #status experimental <LCH>
F; 90-121/Domain: EGF homology <EGL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coagulation factor Xa (EC 3.4.21.6) precursor - chicken
N;Alternate names: virus-activating proteinase
C;Species Gallus Gallus (chicken)
C;Decies Gallus Gallus (chicken)
C;Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text_change 16-Jul-1999
C;Accession: S15838; S20380; $\overline{5}20381$
K;Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na FEBS Lett. 283, 281-285, 1991
A;Title: Primary structure of the virus activating protease from chick embryo. Its ident
A;Reference number: S15838; MUID:91257322; PMID:2044767
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A; Realdues: 1-475 <SUZ>
A; Cross-references: DDBJ:D00844; NID:g222869; PIDN:BAA00724.1; PID:g222870
A; Cross-references: DDBJ:D00844; NID:g222869; PIDN:BAA00724.1; PID:g222870
R; Gotch, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y.
FEBS Lett. 296, 274-278, 1992
A; Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib
A; Reference number: S20380; MUID:92164779; PMID:1537403
A; Acegesion: S20380
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F;46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #8
F;46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #8
F;57-66,90-101,99-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,42
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;196,207,228,285/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;282,328,425/Active site: His, Asp, Ser #status predicted
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F;186-475/Product: coagulation factor X heavy chain #status predicted <HCH>
F;186-240/Domain: activation peptide #status predicted <APT>
F;241-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>
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                                                   F:391-407/Disulfide bonds: #status experimental
F:406,462/Active site: His, Asp #status predicted
F:416/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:568/Active site: Ser #status experimental
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                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 ANTFLEEVRKGNLERECVEETCSYEEAFEALESSTATDVFWAKY 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
F;336-482,536-550,564-594/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                  Query Match 41.0%; Score 82; DB 1; 18est Local Similarity 36.4%; Pred. No. 4.5e-05; Matches 16; Conservative 7; Mismatches 21
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A;Residues: 41-55 <GO2>
A;Accessor
A;Accesor type: protein
A;Molecule type: protein
A;Regidues: 241-246,'X',248-251,'X',253-261 <GOT>
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Best Local Similarity 38.1
Matches 16; Conservative
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Gaps ö

Length 642; 18; Indels

DB 2; 9.8e-05;

40.0%; Score 80; 36.4%; Pred. No.

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MEDLINE-85269639; PubMed-2991859;
Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree G.R.,
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MEDLINE-90293094; PubMed=1694179;
MIDLINE-90293094; PubMed=1694179;
MIDLICHO J.P., Broze G.J. Jr.;
"Beta protein C is not glycosylated at asparagine 329. The rate of translation may influence the frequency of usage at asparagine-X-
PRTC HUMAN STANDARD; PRT; 461 AA. 904070; 015189; 015190; 016001; 01-NOV-1986 (Rel. 03, Last sequence update) 01-NOV-1986 (Rel. 03, Last sequence update) 1-SSRP-2003 (Rel. 42, Last annotation update) 1-SSRP-2003 (Rel. 42, Last annotation update) 1-SSRP-2003 (Rel. Action update) 1-SSRP-2003 (Rel. 
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nucleic Acids Res. 13:5233-5247(1985).
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MEDLINE=85270390; PubMed=2991887;
MOSTER D.C., Yoshitake S., Davie B.W.;
"The nucleotide sequence of the gene for human protein C.";
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MEDLINE-86120978; PubMed=3511471;
Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.;
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J. Biol. Chem. 265:11397-11404(1990).
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MEDLINE=84272714; PubMed=6589623;
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Reliema P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;
"The spectrum of genetic defects in a panel of 40 Dutch families with
symptomatic protein C deficiency type I: heterogeneity and founder
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MEDLINE=97157472; PubMed=9003757;
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Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
Sala N., Cooper D.N.;
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Bovill E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer
Rainville I.R., Long G.L.;
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plasma factor activated protein C and its zymogen.";
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MEDLINE=90098906; PubMed=2602169;
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MEDLINE=92305321; Pubmed=1611081;
                 MEDLINE=92184750; PubMed=1544894;
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MEDLINE=92380660; PubMed=1511988;
                                                                                                                                         3D-STRUCTURE MODELING OF 175-450 MEDLINE=94272342; PubMed=8003977
                                                                                                                                                                                                                                                                                                                                                                 "The 2.8 A crystal structure
EMBO J. 15:6822-6831(1996).
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VARIANTS GLY-14; GLN-211; TYR-244; GLN-253; LEU-321; CYS-328; ILE-385;
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protein C (PROC)
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anticoagulant
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Five novel mutations located in exons III and IX of the protein C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Twelve novel and two recurrent mutations in 14 Austrian families with hereditary protein C deficiency.";
Blood Coagul. Pibrinolysis 4:273-280(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gandrille S., Vidaud M., Aiach M., Alhenc-Gelas M., Fischer A.M., Gouault-Heilman M., Toulon P., Flessinger J.N., Goossens M.; "Two novel mutations responsible for hereditary type I protein C deficiency: characterization by denaturing gradient gel
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MEDLINE=33271391; PubMed=8499565;
Poort S.R.; Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,
Bertina R.M.;
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Kakkar V.V., Cooper D.N.;
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MEDLINE=93313192; PubMed=8324221;
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Blood Coagul. Fibrinolysis 4:345-347(1993)
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MEDLINE=92276939; PubMed=1593215;
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                                                                                                                    Genet. 89:683-684(1992)
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3100d 82:159-168(1993).
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-1- SUBUNT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE BUSYME IS THEN ACTIVATED BY THROWBIN, WHICH CLEAVES A TETAADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROWBOMODILIN.
-!- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-!- PTM: THE VITAMIN K-DEPENDENT, ENTYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
-!- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO SITE IS NECESSARY FOR THE RECOGNITION OF THE THROWBOWODULIN COMPLEX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A comparative study or partie.";
region of mammalian protein C.";
Br. J. Haematol. 86:590-600(1994)
-I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
-I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
-I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
-INCREMENTED BLOOD COAGULATION BY INACTIVATING PACTORS VA
IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
-- PROTEIN FOR THE PROTEIN FOR THE PROSPHOLIPIDS.
                                                                Gaps
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Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
"A comparative study of partial primary structures of the catalytic
                                                                                                                                                                                                                                                               PRTC MOUSE STANDARD; PRT; 461 AA.
P3367; 035498;
01-FEB-1994 (Rel. 28, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
Alcanin-K-dependent protein C precursor (EC 3.4.21.69)
factor XIV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D., Castellino F.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tada N., Sato M., Taujimura A., Iwase R., Hashimoto-Gotoh T., "Isolation and characterization of a mouse protein C cDNA."; J. Biochem. 111:491-495(1992).
                     Length 461;
                                                             10; Indels
                                                                                                             44
                                                                                                                                   1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                ch 84.0%; Score 168; DB 1; Similarity 72.7%; Pred. No. 6.1e-21; 32; Conservative 2; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thromb. Haemost. 79:310-316(1998)
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MEDLINE=98152576; PubMed=9493582;
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SEQUENCE OF 274-434 FROM N.A.
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Best Local Similarity
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R PROSITE; PS01187; EGF_CA; 1.

R ROSITE; PS0011; GLU_CARBOXYLATION; 1.

R RROSITE; PS00134; TRYPSIN_HIS; 1.

R ROSITE; PS00134; TRYPSIN_HIS; 1.

R ROSITE; PS00135; TRYPSIN_HIS; 1.

R ROSITE; PS00135; TRYPSIN_SER; 1.

W Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation; KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation; FT SIGNAL 1 33 BY SIMILARITY.

FT PROPEP 34 41 BY SIMILARITY.

FT CHAIN 199 461 PROTEIN C LIGHT CHAIN (BY SIMILARITY).

FT CHAIN 199 212 ACTIVATION PEPTIDE (BY SIMILARITY).

FT PEPTIDE 199 212 ACTIVATION PEPTIDE (BY SIMILARITY).
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as its content is in no
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GAMMA-CARBOXYGLUTAMIC ACID
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(BY SIMILARITY).

(BY SIMILARITY).

GAMMA-CARBOXYGLUTAMIC ACID

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TE; PS00010; ASX HYDROXYL; 1.
TE; PS00128; EGF 1; 1.
TE; PS01186; EGF 2; 2.
TE; PS01197; EGF CA; 1.
TE; PS00111; GLU CARBOXYLATION; 1.
TE; PS00211; GLU CARBOXYLATION; 1.
                                                                                                                                                                                                                                                                    InterPro; IPR006209; EGF_Iike.
InterPro; IPR001283; GLA_blood.
InterPro; IPR001284; SCI_Drotease_Try.
InterPro; IPR001294; VitK_dep_GLA_Fam; PP00008; EGF; 2.
Fam; PP000089; EGF; 2.
Fam; PP000089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR0001; GLABLOOD.
SMART; SM000179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
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InterPro; IPR001314; Chymotrypsin.
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EGF_like.
GLA_blood.
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MGD; MGI:97771; Proc.
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HSSP; P04070; 1PCU.
MEROPS; S01.218; -.
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    -!-SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE BUZYME IS THEN ACTIVATED BY THROMEIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTOED BY THROMBOMODULIN.
-!- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-!- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
-- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECCRITION OF THE TROMBIN-THROMBOMODULIN COMPLEX.
-!- SIMILARITY: BELONGS TO PERTINASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS.PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN Wister; TISSUE-Liver;

MEDLINE-92329550; PubMed=1627650;

MEDLINE-92329550; PubMed=1627650;

MEDLINE-92329550; PubMed=1627650;

MEDLINE-92329550; PubMed=1627650;

Charly T., Maekawa K., Nawa K., Marumoto Y.;

Biochim. Biophys. Acta 1131:329-332(1992).

-! FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.

-! CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCbl_TaxID=10116;
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                            Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
factor XIV).
                                                                                      . .) (POTENTIAL).
. .) (POTENTIAL).
. .) (POTENTIAL).
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                                                                                                                                                                 Score 139; DB 1; Length 461;
Pred. No. 5.8e-16;
7; Mismatches 11; Indels
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01-JUL-1993 (Rel. 26, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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hes 26; Conservative
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                                                                                                                                              461 AA;
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68.5%; Score 137; DB 1; Length 458;
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  -!- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A FETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.
-!- TISSUE SPECIFICITY: PLASNA; SYNTHESIZED IN THE LIVER.
-!- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLU RESTDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCTUM.
-- MISCELLANEOUS: CALCTUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECCENTION OF THE THROMBOMODULIN COMPLEX.
-!- SIMILARITY: BELONGS TO PEFFINES. FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                         Shen L., He X., Dahlback B.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REQULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                      Gaps
                                                                                                                                                                                          PRTC RABIT

ID PRTC RABIT

ID PRTC RABIT

STANDARD; PRT; 458 AA.

15-0661;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Vitemin-K-dependent protein C precursor (EC 3.4.21.69)

DE (Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation DE factor XIV) (Fragment).
                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
           BY SIMILARITY. (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                              Score 138; DB 1; Length 461;
Pred. No. 8.7e-16;
                                                                                                     11; Indels
                                                                                                                            1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                        8A4CF93664EDACD5 CRC64;
                                                                                                                                         7; Mismatches
  SIMILARITY
                                                                               Score 138;
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001881; EGF _Ga.
InterPro; IPR006209; EGF like.
InterPro; IPR002383; GLA_blood.
387 BY
426 BY
215 N-
291 N-
355 N-
51912 MW;
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                                                                               69.08;
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                                                                                                      Conservative
 373
398
215
291
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461 AA,
                                                                                        1 Similarity
26; Conserv
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TISSUE=Liver;
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BY SIMILARITY.

BY SIMILARITY.
VITAMIN K-DEPENDENT PROTEIN C.
PROTEIN C LIGHT CHAIN (BY SIMILARITY).
ACTIVATION PEPTIDE (BY SIMILARITY).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
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(GLCNAC. .) (POTENTIAL)
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
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(BY SIMILARITY).
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GAMMA-CARBOXYGLUTAMIC ACID
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GAMMA-CARBOXYGLUTAMIC ACID
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GAMMA-CARBOXYGLUTAMIC ACID
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GAMMA-CARBOXYGLUTAMIC ACID
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                                                                                                                                                                                                                                                                                 Blood coagulation; Glycoprotein; Serine protease;
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                                                                                                       SMART; SM00181; EGF; 2.
SMART; SM00181; EGF; 2.
SMART; SM00069; GLA; 1.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS01022; EGF 1; 1.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS00011; GLU CARBOXYLATION; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
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EGF-LIKE 2.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00009; EGF; 2.
Pfam; PF000894; gla; 1.
Pfam; PF00089; trypshi, 1.
PRINTS; PR00022; CTYMOTRYESIN.
PRINTS; PR00001; GLABLOOD.
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52.3%;
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PF00089; trypsir
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459 AA;
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Best Local Similarity
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          Pfam;
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 -1- SUBDNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promomodulin.

-I TISSUE SPECIFICITY: Planas; synthesized in the liver.
-I- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.
-I- MISCELLANBOUS: Calcium also binds, with stronger affinity to another site, beyond the GlA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.
-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                          MEDLINE=21121490; PubMed=11229814;
Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
Kim H.K.W.;
           Gaps
                                                                                                    16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Vitamin-K-dependent protein C precursor (BC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
                                                                                                                                                                        Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Pred. No. 1.3e-15;
4; Mismatches 14; Indels
                             44
                                        37 ANSFLEELRPSSLERECVEEVCDLEEAKEIFOSVDDTLAFWYKY 80
                            1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                             459 AA.
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VitK_dep_GLA.
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InterPro; IPR001314; Chymotrypsin.
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EGF like.
GLA blood.
IEGF.
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59.1%;
         26; Conservative
                                                                                             STANDARD;
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Best Local Similarity
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PRTC_PIG
TO PRTC_PIG
Q9GLP2;
          Matches
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ACTIVATION PEPTIDE (BY SIMILARITY).
CLEAVAGE (BY THROMBIN) (BY
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SAMMA-CARBOXYGLUTAMIC ACID (BY
SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID (BY
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GAMMA-CARBOXYGLUTAMIC ACID (BY
SIMILARITY).
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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Pred. No. 4.8e-13;
                                                                                                                                                                                                                                                                                                                                                                                              SERINE PROTEASE
                                                                                                                                                                                                                                                                                     SIMILARITY)
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51866 MW;
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SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPERTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-83213514; PubMed=6405503;
MEDLINE-83213514; PubMed=6405503;
Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;
Structural changes required for activation of protein C are induced by Ca2+ binding to a high affinity site that does not contain gamma-carboxyglutamic acid.";
J. Biol. Chem. 258:5554-5560(1983).
-I- FUNCTION: PROTEIN C IS A.VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIOS.
-I- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
  Gaps
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-886014826; PubMed-6091100;
Long G.L., Balagaje R.M., McGillivray R.T.A.;
"Cloning and sequencing of liver cDNA coding for bovine protein C.";
Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 197-456, AND CARBOHYDRATE-LINKAGE SITES ASN-289; ASN-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=83213513; PubMed=6304092;
Esmon N.L., Debault L.E., Esmon C.T.;
"Proteolytic formation and properties of gamma-carboxyglutamic acid-
                                                                                                                               21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1987 (Rel. 42, Last annotation update)
Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).
                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-83169769; PubMed=6572939;
Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
"Beta-hydroxyaspartic acid in vitamin K-dependent protein C.";
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MEDLINE=83007326; PubMed=6896877;
Stenflud P.;
Stenflud scid sequence of the heavy chain of bovine protein C.";
J. Biol. Chem. 257:12180-12190(1982).
                                                                                                                                                                                                                                                                                                                                                                                        Fernlund P., Stenflo J.; "Amino acid sequence of the light chain of bovine protein C."; J. Biol. Chem. 257:12170-12179(1982).
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MEDLINE-83007325; PubMed-6896876;
 14; Indels
                                    ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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 7; Mismatches
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23; Conservative
                                                                                                         STANDARD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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SIGNAL <1 29
PROPEP 30
                               -!- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-!- PTM: THE VITAMIN K-DEPRNDENT, ENZYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFED PROTEIN TO BIND CALCIUM.
-!- MISCELLANBOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECCGNITION OF THE THROMEIN-THROMBONDULIN COMPLEX.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
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CHARGE RELAY SYSTEM
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PROSITE; PSUGUAS; EGF_2; 2.
PROSITE; PSUGUA7; EGF_CA, 1.
PROSITE; PSUGUA7; EUFFERDXYLATION; 1.
PROSITE; PSUGUA0; TRYPSIN DOM; 1.
PROSITE; PSUGUA0; TRYPSIN LIS; FALSE_NEG.
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InterPro; IPR002891; EGF_Ca.
InterPro; IPR002393; GLA_blood.
InterPro; IPR002301; IEGF_Like.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
IPEan; PP00594; Gla; 1.
PEan; PP00089; ETYPain; 1.
PENNTS; PR007022; GHYMOTRYPSIN.
PRINTS; PR007021; GLABLOOD.
STRONGLY PROMOTED BY THROMBOMODULIN
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SMART; SM00069; GLA; 1.
SMART; SM00020; TYP2 SPC; 1.
PROSITE; PS00010; AST HYDROXYL; 1.
PROSITE; PS00022; EGF_1; 1.
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Chymotrypsin.
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InterPro; IPR001314;
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MEROPS; S01.218; -.
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Natl. Acad. Sci. U.S.A. 72:3082-3086(1975)
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J. Biol. Chem. 267:19642-19649(1992).
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                                             MEDLINE=94062825; PubMed=8243461;
Inoue K., Morita T.;
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MEDLINE-76053069; PubMed=1059093;
Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
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MEDLINE=84247315; PubMed=6330671;
Fung M.R., Campbell R.M., McGillivray R.T.A.;
"Blood coagulation factor X mRNA encodes a single polypeptide chain
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NCBI_TaxIb=9913,
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MEDLINE=80130563; PubMed=6766735;
Enfield D.L., Ericsson L.H., Pujikawa K., Walsh K.A., Neurath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
43-AUG-1987 (Rel. 05, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor)
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Pred. No. 7.1e-13;
9; Mismatches 12; Indels
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CAAF6833F894C209 CRC64;
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Biochem. Biophys. Res. Commun. 115:8-14(1983)
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Nucleic Acids Res. 12:4481-4492(1984).
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MEDLINE=91084483; PubMed=2261466; Selander M., Persson E., Stenfilo J., Drakenberg T.; However the selander M. However and secondary structure of the Ca2(+)-free form of the amino-terminal epidermal growth factor like domain in coagulation
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EGF-
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Eur. J. Biochem. 218:153-163(1993).
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"Bovine factor X la (activated Stuart factor). Bvidence of homology
with mammalian serine proteases.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Fitani K., Hermodson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
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Sugo T., Bjoerk I., Holmgren A., Stenflo J.;
Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic acid-containing region.";
J. Biol. Chem. 259:5705-5710(1984).
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Selander-Sunnerhagen M., Ullner M., Persson E., Teleman O.,
Stenfilo J., Drakenberg T.;
"How an epidermal growth factor (BGF)-like domain binds calcium.
resolution NMR structure of the calcium form of the NH2-terminal
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MEDLINE-96387194; PubMed-8794734;
Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
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"Activation of bovine factor X (Stuart factor): conversion of
"Axa-alpha to factor Xa-beta.";
Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
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Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES
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      FUNCTION: Pactor Xa is a vicamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.

CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then Arg-|-Ile bonds in prothrombin to form thrombin.

BY THE EXCISION OF TWO RAE FORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR MORE DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PACTOR X LIGHT CHAIN.

PACTOR X HEAVY CHAIN.

ACTIVATION PEPTIDE.

ACTIVATED FACTOR XA, HEAVY CHAIN.

MAY BE REMOVED BUT IS NOT NECESSARY FOR ACTIVATION.
                                                                                                      PTM: N- AND O-GLYCOSYLATED.

PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY PACTOR IXA (IN THE INTRINSIC PATHWAY).

MISCELLANESIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).

MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOWNIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

SIMILARITY: Contains 2 EGP-like domains.
                                                                               SOME
                                                                             PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SC
GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
                                                                                                                                                                                                                                                                                                                                GlycoSuiteDB; P00743; -.
InterPro; IPR00152; Asx hydroxyl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR00142; EGF 2.
InterPro; IPR001881; EGF 72.
InterPro; IPR00289; EGF 1ike.
InterPro; IPR002383; GLA_blood.
InterPro; IPR002545; Ser_protesse_Try.
InterPro; IPR002294; VitK_dep_GLA.
Biochemistry 35:11547-11559(1996)
                                                                                                                                                                                                                                                   EMBL; X00673; CAA25286.1;
PIR; A22867; EXBO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
492
492
492
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1 CCF; 31-MAY-94.
1 LWHE; 15-MAY-97.
1 WHF; 15-MAY-97.
1 LOD; 21-JAN 03.
                                                                                                                                                                                                                                                                                                                          MEROPS; S01.216;
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183
183
234
476
                                                                                                CALCIUM.
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PROPEP
CHAIN
PROPEP
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PDB;
PDB;
          <u>:</u>
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SEQUENCE FROM N.A.
MEDLINE=91216473; PubMed=1902434;
Mesaier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
"Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagulation factor X.";
Gene 99:291-294(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
BGF-LIKE 1, CALCIUM-BINDING (POTENTIAL) BGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=86221713; PubMed=3011603;
Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
"Isolation and characterization of human blood-coagulation factor X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=85216545; PubMed=2582420;
Fung M.R., Hay C.W., McGillivray R.T.A.;
"Characterization of an almost full-length cDNA coding for human blood coaqulation factor X.";
proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=87026600; PubMed=3768336;
Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
"Gene for human factor X: a blood coagulation factor whose gene organization is essentially identical with that of factor IX and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Czuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAIO_HUMAN STANDARD; PRT; 488 AA.
P00742; Q14340;
21-JUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 109; DB 1; Length 492;
Pred. No. 8.9e-11;
                                                           SERINE PROTEASE.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
GAWMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Indels
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McMullen B.A., Pujikawa K., Kisiel W., Sasagawa T., Howald W.N., Kwa B.Y., Weinstein B.; "Complete amino acid sequence of the light chain of human blood coagulation factor X: evidence for identification of residue 63 as beta-hydroxyaspartic acid."; Biochemistry 22:2875-2884(1983).
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93360277; PubMed=8355279;
Padmanabhan K.P., Tulinsky A., Park C.H., Bode W., Huber R., Blankenship D.T., Cardin A.D., Kisiel W.;
"Structure of human des(1-45) factor Xa at 2.2-A resolution.";
                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-23 FROM N.A.
MEDIINE=90128299; PubMed=2612918;
Agaddeswaran P., Reddy S.V., Rao K.J., Hamsabhushanam K., Lyman "Cloning and characterization of the 5' end (exon 1) of the gene encoding human factor X.";
                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
                                                                                                                          MEDLINE=84222026; PubMed=6587384;
Leytus S.P., Chung D.W., Xisiel W., Kurachi K., Davie )
"Characterization of a CNA coding for human factor X.
Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
                                                                                                    SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998)
                                                                                                                                                                                                                                                                    Eur. J. Biochem. 218:153-163(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Biol. 232:947-966(1993).
[11]
MEDLINE=83257207; PubMed=6871167
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                                                                                                                                                                                                                                                                                                                                                           Gene 84:517-519(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of human genes."
                                                                                                                  TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lander E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          actor Xa.";
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-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-1- SIMILARITY: CONCAINS 2 EGF-like domains. GO; GO:0005576; C:extracellular; TAS.
GO; GO:0003804; F:blood coagulation factor X activity; TAS.
GO; GO:0007596; P:blood coagulation; TAS. InterPro; IRR00152; Asx hydroxyl.
InterPro; IPR0011314; Chymctrypsin.
InterPro; IPR0011314; Chymctrypsin.
InterPro; IPR001431; EGF_2.
InterPro; IPR001431; EGF_II.
InterPro; IPR001431; EGF_II.
InterPro; IPR002031; EGF_II.
InterPro; IPR002031; GIA_blood.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001254; Vitk_dep_GIA.
InterPro; IPR000294; Vitk_dep_GIA.
IPR000089; IrryPsin; IPR001294; Vitk_dep_GIA.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00010; EGFBLOOD.
SWART; SM00179; EGF (A; I. JOINED. JOINED. JOINED. L00390; AAA52764.1; JOINED EMBL; K03194; AAA52490.1; -. EMBL; M57285; AAA52421.1; -. AF503510; AAM19347.1; SM00020; Tryp_SPc; 1 L29433; AAA52764.1; L00391; AAA52764.1; L00392; AAA52764.1; AAA52764.1; AAA52486.1; AAA52636.1; AAA52764.1; AAA52764.1; AAA52764.1; AAA51984.1; PDB; 1NFY; 25-FEB-03. MEROPS; S01.216; -. GlycoSuiteDB; P00742; Genew; HGNC:3528; F10. 08-MAY-95. 29-OCT-97. 17-JUN-98 20-SEP-00 19-JUN-02 25-FEB-03 0-SEP-20-0CT-K01886; M33297; L00395; M22613; гооз96; A24478; 1MQ5; 1MQ6; 1NFU; HCG; 1KSN; 1KYE; 1XKB; POS; 1G2L; 1NFX; FXY; XKA; 1EZO; FJS; 1NFW; SMART; EMBL; PIR; PDB; ٠. Lander E.S.; "Characterization of single-nucleotide polymorphisms in coding regions Genet. 23:373-373(1999).
FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.
CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-rhr and then Arg-|-rle bonds in prothrombin to form thrombin.
SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR MORE DISULFIDE BONDS. SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
MEDLINE=94062825; PubMed=8243461;
Inoue K., Morita T.;
"Identification of O.linked oligosaccharide chains in the activation peptides of blood coagulation factor X. The role of the carbohydrate moieties in the activation of factor X."; .. G MEDLINE=98283982; PubMed=9618463; Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.; "Structural basis for chemical inhibition of human blood coagulation MEDLINE=99318093; PubMed=10391209; Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L. Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q., Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L. Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q., TISSUE SPECIFICITY: Plasma; synthesized in the liver.
PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
PTM: N- AND O-GLYCOSYLATED. .. ₩.:

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PRINTS;
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                                                                                                                                  FA10_RABIT
                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.0%; Score 102; DB 1; Length 231; 41.5%; Pred. No. 5.9e-10;
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1 Similarity 43.2%; Pred. No. 1.3e-10;
19; Conservative 8; Mismatches 17. Tadal
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                                                                                                                                                                                                                                                                                    1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                  PROTEIN 3.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 EXTRACELLULAR (POTENTIAL).
21 POTENTIAL.
231 CYTOPLASMIC (POTENTIAL).
60 GLA-RICH.
25848 MW; 8A373E4848490D81 CRC64;
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PROPEP
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GO; GO:0016021; C:integral to membrane; NAS.
InterPro; IPR001294; VitK_dep_GLA.
Pfam; PR00594; gla; 1.
PRART; SM00069; GLA; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 AA
                                                                   EGF_CA, 1.
GLU_CARBOXYLATION, 1.
  ASX HYDROXYL; 1
                                                                                                                            PS50240; TRYPSIN DOM; 1.
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les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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TISSUE=Spinal cord;
                           PS00022;
PS01186;
PS00010;
                                                                              PS01187;
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PROSITE; E
PROSITE; E
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SEQUENCE
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TMG3_HUMAN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                MEDLINE=9726311; PubMed=9101642;
Pendurthi U.R., Anderson K.D., James H.D.;
Pendurthi U.R., Anderson K.D., James H.D.;
Pendurthi U.R., Anderson K.D., James H.D.;
Thromb. Res. 85:803-514(1997).
-!- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.
-!- CATALYIIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then Arg-|-Ib bonds in prothrombin to form thrombin.
-!- SUBUNIT: THE TWO CHAINS ARE PORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MORE DISULFIDE BONDS.

PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).

PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).

PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- MISCELLANGOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
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20 ANEFLEELRQGTIERECMEEICSYEEVKEVPENKEKTMEFW
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InterPro; IPR01881; EGF Ca.
InterPro; IPR001438; EGF II.
InterPro; IPR006209; EGF III.
InterPro; IPR002383; GLA blood.
InterPro; IPR001254; Ser_protease Try.
InterPro; IPR001294; VitK_dep_GLA.
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SMART; SM00069; GLA; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chymotrypsin.
EGF 2.
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PRINTS; PR00722; CHYMOTRYPSIN.
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                                                                                                                   STANDARD;
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Pfam; PF00594; gla; 1
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                                                                                                                 FA10 RABIT
019045;
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PROSITE; PS00022; EGF 1; 1.

PROSITE; PS01186; EGF 2; 2.

PROSITE; PS01181; EGF CA; 1.

PROSITE; PS00011; GLU_CARBOXYLATION; 1.

PROSITE; PS00013; TRYPEIN_HIS; 1.

PROSITE; PS00134; TRYPEIN_HIS; 1.

Glycoprotein; Hydrolase; Serine pyrotease; Plasma; Blood coagulation; Gamma-carboxygluteanic acid; Hydroxylation; Calcium-binding; Vitamin K; Signal; Zymogen; EGF-like domain; Repeat.,
                                                                                                     FACTOR X LIGHT CHAIN.
FACTOR X HEAVY CHAIN.
ACTIVATION PEPTIDE.
ACTIVATED FACTOR XA, HEAVY CHAIN.
EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
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BY SIMILARITY.
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
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   Length 490;
 Score 101; DB 1; Length 49
Pred. No. 2.1e-09;
8; Mismatches 17; Indels
                                                                     1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Query Match
Best Local Similarity 43.2%;
Matches 19; Conservative
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41

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RESULT 11

SM00020; Tryp_SPc; 1

SMART;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                    Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.,
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FA7 RABIT STANDARD; PRT; 444 AA.
P98139; P79224;
01-FEB-1996 (Rel. 33, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           form factor Xa.

-!- SUBNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
BY A DISULPIDE BOND (BY SIMILARITY).

-!- TISSUE SPECIFICITY: Plasma.

-!- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CALCIUM (BY SIMILARITY).

-!- SIMILARITY: BELOAGS TO PEPFIDASE FAMILY S1.

-!- SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-11e bond in factor X
                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR000742; EGF 2.
Interpro; IPR011881; EGF Ca.
Interpro; IPR001438; EGF Ti.
Interpro; IPR005209; EGF Tike.
Interpro; IPR002383; GLA_blood.
Interpro; IPR002383; GLA_blood.
Interpro; IPR000254; Ser_protease_Try.
Interpro; IPR000294; VitK_dep_GLA.
Pfam; PF00594; gla; 1.
                                                                                                                                                                                                                                                                                                Thromb. Res. Suppl. 69:231-238(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chymotrypsin.
EGF 2.
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                                                                                                                                                                                                                                    MEDLINE=93190306; PubMed=8383365;
                                                                                                                             Oryctolagus cuniculus (Rabbit)
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PRINTS, PR00122; CHYMOTRYPSIN.
PRINTS; PR00010; ECPELOOD.
PRINTS; PR00001; GLABLOOD.
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SMART; SM00179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
                                                                                                conversion accelerator)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nterPro; IPR001314;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                       NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                                                                           TISSUE=Liver;
                                                                                                                                                                                                                     TISSUE=Liver
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PROPEP SIGNAL

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MEDLINE=91344709; PubMed=2129367; Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.; Manimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.; M. and wrisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z."; Adv. Exp. Med. Biol. 281:121-131(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Amino acid sequence and posttranslational modifications of human factor VIIa from plasma and transfected baby hamster kidney cells."; Biochemistry 27:7785-7793(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99126538; PubMed=9925787;
Zhang E., St Charles R., Tulinsky A.;
"Structure of extracellular tissue factor complexed with factor VIIa
inhibited with a BPTI mutant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
MEDILNE-8908B153; PubMed=1264725;
Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
Pedersen A.H., Hedner U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90062160; PubMed=2511201;
Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T., Shimonishi Y., Iwanaga S.; Kisiel W., Hase S., Ikenaka T., Takao T., Identification of a disaccharide (Xyl-Glc) and a trisaccharide (Xyl2-Glc) O-glycosidically linked to a serine residue in the first epidermal growth factor-like domain of human factors VII and IX and Drottein Z., M. Biol. Chem. 264:20320-20325(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Banner D.W., D'Arcy A., Chene C., Winkler P.K., Guha A.,
Konigsberg W.H., Nemreson Y., Kirchhofer D.;
The crystal structure of the complex of blood coagulation factor
"The soluble tissue factor.";
Nature 380:41-46(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF
     , Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                 MEDLINE=87260948; PubMed=3037537;
O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
Hagen F.S., Murray M.J.;
"Nucleotide sequence of the gene coding for human factor VII, a
vitamin K-dependent protein participating in blood coagulation.",
Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445. Rieder M.J., Armel T.Z., Cartington D.P., Chung M.-W., Lee K.L., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
MEDLINE=91250411; PubMed=1994059;
Bjoern S., Foster D.C., Thim L., Wiberg F.C., Christensen M., Komlyama Y., Pedersen A.H., Kisiel W.;
"Human plasma and recombinant factor VII. Characterization of (glycosylations at serine residues 52 and 60 and effects of site directed mutagenesis of serine 52 to alanine.";
J. Biol. Chem. 266:11051-11057(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH MEDLINE-96175641; Pubmed-8598903;
                                                                                                                          Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C., Woodbury R.G., Hart C.E., Insley M.Y., Kisiel W., Kurachi K.,
                                                                                                                                                                               "Characterization of a cDNA coding for human factor VII.";
Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
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                                                                                       TISSUE=Liver;
MEDLINE=86205965; PubMed=3486420;
     Eukaryota; Metazoa;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                           SEQUENCE FROM N.A.
                       Mammalia; Eutheri
NCBI_TaxID=9606;
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                                                                                                                                                                 Davie E.W.;
     ö
                  PROSTTE; PS00022; EGF 1; 1.
PROSTTE; PS01186; EGF CA; 1.
PROSTTE; PS01187; EGF CA; 1.
PROSTTE; PS00011; GLU CARBOXYLATION; 1.
PROSTTE; PS000134; TRYPSIN_DOM; 1.
PROSTTE; PS000134; TRYPSIN_BER; 1.
PROSTTE; PS00135; TRYPSIN_BER; 1.
Hydrolase; Serine procease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plagma; Vitemin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat; Signal; Hydroxylation.
                                                                                                                                                                                                                                                                                                                            FACTOR IXA, OR THROMBIN) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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EGF-LIKE 2.
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P08709; Q14339;
01-JAN-1988 (Rel. 06, Last sequence update)
01-JAN-1988 (Rel. 06, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (Eptacog alfa).
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(GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
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CARMAA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
HYDROXILATION (BY SIMILARITY).
N-LINKED (GLCNAC.)) (POTENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 100; DB 1; Length 444;
Pred. No. 2.8e-09;
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SUBSTRATE (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                     SERINE PROTEASE.
CLEAVAGE (BY FACTOR XA,
                                                                                                                                                                                                                               FACTOR VII LIGHT CHAIN. FACTOR VII HEAVY CHAIN.
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ASX_HYDROXYL; 1.
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Best Local Similarity 46.3%;
Matches 19; Conservative
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444 AA;
PS00010;
PS00022;
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DISULFID
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deficiency causes defective secretion of the molecule.";
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MEDLINE=95072589; PubMed=7981691;
MEDLINE=95072589; PubMed=7981691;
MEDLINE=95072589; PubMed=7981691;
Redeghiero F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
Rodeghiero F., Merletti G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94264305; PubMed-8204879; Chaing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W., Roberts H.R., Blajchman M., Monroe D.M., High K.A.; Severe factor VII deficiency caused by mutations abolishing the cleavage site for activation and altering binding to tissue factor."; Blood 83:3524-3535 (1994).
                                                                                                                                                                                                                                                   VARIANT GLN-364.

MEDLINE=9130006; PubMed=2070047;
O'Barien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
Meade T.W., Tuddenham E.G.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ል
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MEDLINE=96247510; PubMed=8652821;
Arbini A.A., Mannucci P.M., Bauer K.A.;
"A Thr359Met mutation in factor VII of a patient with a hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caused
                                                                                                                                                       'Solution structure of the N-terminal EGF-like domain from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WEDLINE 94061028; PubMed=8242057;
Takamiya O., Kemball-Cook G., Martin D.M.A., Cooper D.N.,
von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
Tuddenham E.G.D., McVey J.H.;
"Detection of miseense mutations by single-strand conformational
polymorphism (SSCP) analysis in five dysfunctional variants of
coagulation factor VII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93372811; PubMed=8364544;
Marchetti G., Ferrati M., Patracchini P., Redaelli R., Bernardi M. a misense mutation (178Cys-->Tyr) and two neutral dimorphisms (115His and 333Ser) in the human coagulation factor VII gene."; Hum. Mol. Genet. 2:1055-1056(1993).
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MEDLINE-981367502, Pubmed=9692950;
Muzanyi A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,
Drakenberg T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95064662; PubMed-7974346;
Ohlwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS CHARLOTTE GLN-139 AND GLN-212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Genet. 2:1355-1359(1993)
                                                                                                                                                                            factor VII.";
Biochemistry 37:10605-10615(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92340074; PubMed=1634227;
  Mol. Biol. 285:2089-2104 (1999)
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"Characterization of single-nucleotide polymorphisms in coding regions
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28-FEB-2003 (Rel. 41, Last annotation update)
Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97037613; PubMed=8883260;
MEDLINE=97037613; PubMed=8883260;
Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
Zaizov B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
"Aladyaval is a common, probably ancient mutation causing factor VII
deficiency in Moroccan and Iranian Jews.";
Thromb. Haemost. 76:283-291(1996).
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MEDLINE-99318093; Pubmed=10391209;
Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
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                                                                                              VARIANTS TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413. MEDLINE-97001216; PubMed-8844208; Bernard F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G., Lunghi B., Rodeghiero F., Marchetti G.; Mutation pattern in clinically asymptomatic coagulation factor VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Factor VII Morioka (FVII L-26P): a homozygous missense mutation in the signal sequence identified in a patient with factor VII deficiency.";
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alshinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E., "Two new missense mutations (P134T and A244V) in the coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Sakuragawa N.;
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Mutat. Suppl. 1:S189-S191(1998)
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MEDLINE=98112461; PubMed=9452082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98235713; PubMed=9576180;
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MEDLINE=97404347; PubMed=9256434;
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28-FBB-2003 (Rel. 41, Last seq
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Conservative
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Blood 87:5085-5094 (1996).
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        "Primary structure and tissue distribution of two novel proline-rich gamma-carboxyglutamic acid proteins.";
Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997)
- I TISSUE SPECIFICITY: Highly expressed in the spinal cord.
- I PTM: Gla residues are produced after subsequent posttranslational modifications of glutamic acid by a vitamin K-dependent gamma-
                                                                                                                                                                                                                                                                                                                                TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Mětazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 43.5%; Score 87; DB 1; Length 218; 36.4%; Pred. No. 2.1e-07;
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                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
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Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
PROPEP
                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
CYTOPLASMIC (POTENTIAL)
GLA-RICH.
 Davie E.W.;
                                                                                                                                                                                                                    MIM; 604428; -. C.integral to plasma membrane; TAS. 60; GO:0005887; C.integral to plasma membrane; TAS. InterPro; IPR002383; GLA blood.
InterPro; IPR000294; Vitk_dep_GLA.
Pfam; PF00594; glas; 1.
PRINTS; PR00001; GLABLCOD.
SMART; SM00069; GLA: 1.
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01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Prothrombin precursor (EC 3.4.21.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Mismatches
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Kulman J.D., Harris J.E., Haldeman B.A.,
                                                                                                                                                                                                                                                                                                                                            PROTEIN 1
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Nucleic Acids Res. 18:4251-4251(1990)
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MEDLINE-90332426, PubMed-2377469,
Dihanich M., Monard D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                           24947 MW;
                                                                                                                                                                                    EMBL; AF009242; AAB67070.1; -.
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                                                                                                                                                                                                        Genew; HGNC:9469; PRRG1.
MIM; 604428; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Conservative
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106
218
61
135
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                                                                                                                                                                                                                                                                                                                                                                                                           218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                          carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THRB RAT
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P182<u>9</u>2
                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
THRB_RAT
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                amplification and sequence analysis of the B chain of thrombin from nine different species.";

Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).

Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).

FIBRINGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII, AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.

CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates fibrinogen to fibrin and releases fibrinopeptide A and B.

FIM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS, RESULT FROM THE CANBOXYLASE FALTHE MODIFIED SEA MICROSOMAL ENZYMS, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY CHARGED MUSHOLIED SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION OF DEAPLEMENT OF DEAPLEMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF PROTHROWSIN TO THROMBIN.

MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN & FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT & HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE PACTOR VITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00069; GLA; 1.
SMART; SM00060; GLA; 1.
SMART; SM00130; KR; 2.
SMART; SM00130; KR; 2.
SMART; SM00130; KR; 2.
SMART; SM00130; KR; 2.
PROSITE; PS00011; GLÜ CARBOXYLATION; 1.
PROSITE; PS00013; KRINGLE_1; 2.
PROSITE; PS00134; TRYPSIN, DOM; 1.
PROSITE; PS00135; TRYPSIN, DOM; 1.
PROSITE; PS00135; TRYPSIN, SER; 1.
Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
Hydrolase; Serine protease; Kringle; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVATION PEPTIDE (FRAGMENT 1).
ACTIVATION PEPTIDE (FRAGMENT 2).
THROMBIN LIGHT CHAIN (A).
characterization of vertebrate prothrombin cDNAs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      !- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. !- SIMILARITY: Contains 2 kringle domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTHROMBIN.
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InterPro; IPR002383; GLA blood.
InterPro; IPR000001; Kringle.
InterPro; IPR003966; Prothrombin.
InterPro; IPR001254; Ser protease_Try.
InterPro; IPR001294; VitK_dep_GLA.
InterPro; IPR00594; glas; 1.
Pfam; PF000594; glas; 1.
Pfam; PF000594; kringle; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO072; CHYMOTRYBEIN.
PRINTS; PRO001; GLABLOOD.
PRINTS; PRO018; KRINGLE.
PRINTS; PRO155; PROTHROWBIN.
PRODOM; PD000395; Kringle; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X52835; CAA37017.1; -. EMBL; M81397; AAA42240.1; -. PIR; S10511. $10511. HSSP; P00734; 1UVS. MEROPS; S01.217; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200
323
359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THROMBIN.
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PEPTIDE
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Banfield D.K., Macgillivray R.T.;
                                                                                                                                                                           THROMBIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vitamin K; Z
Hydrolase; S
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
ij
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
NCBI_TaxID=10090;
                                                    (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                         . . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=CS/BL/6; TISSUE=Liver;
MEDLINE=91025551; PubMed=222810;
Friezner Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G.,
Fitzgibbon J.J., Pai J.-A., Chapman V.M., Elliott R.W.;
Fitzgibbon J.J., Pai GNA coding for mouse prothrombin and
localization of the gene on mouse chromosome 2.";
DNA Cell Biol. 9:487-498(1990).
                                                                                                                                                                                                                                                                                                     42.2%; Score 84.5; DB 1; Length 617; 42.2%; Pred. No. 1.8e-06;
                                                                          GAMMA-CARBOXYGLUTAMIC ACID.
A-LINKED (GLCNAC...) (POTEN
N-LINKED (GLCNAC...) (POTEN
N-LINKED (GLCNAC...) (POTEN
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                              44 ANSGFLEELRKGNLERECVEEQCSYEEAFEALESPQDTDVFWAKY 88
                                                                                                                                                                                                                                                                                                                                     1 ANS-FLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                     AD27D1B71445DB1D CRC64;
THROMBIN HEAVY CHAIN (B)
                             CLEAVAGE (BY THROMBIN).
CLEAVAGE (BY FACTOR XA)
CLEAVAGE (BY FACTOR XA)
                                                    CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Prothrombin precursor (EC 3.4.21.5).
              KRINGLE 2.
SERINE PROTEASE.
                                                                                                                                                                                                                                                             SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 384-618 FROM N.A.
TISSUE-Liver;
MEDLINE-92212913; PubMed=1557383;
                                                                                                                                                                                                                                                                                      70411 MW;
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 42.27
                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                     617 AA;
THRB MOUSE
ID THRB MOUSE
AC P19221;
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CARBOHYD
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MOD_RES
MOD_RES
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The different species. The species of the B chain of thrombin from amplification and sequence analysis of the B chain of thrombin from nine different species. The different species. The different species. The different species. The species of the brown of the species. The proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).

1- FUNCTION: THROMBIN, WHICH CLEAVES BONDS AFTER ARG & LYS, CONVERTS FARDINGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII, AND, IN COMPLEX WITH THROMBONDOULLIN, PROTEIN C. THIN, XIII, AND, IN COMPLEX WITH THROMBONDOULLIN, PROTEIN C. THE GALLYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates thibrinogen to fibrin and releases fibrinopeptide A and B. THE GAMMA-CARBOXYGLUTAMYL RESIDUES. WHICH BIND CALCIUM IONS, RESULT FROM THE CARBOXYGLUTAMYL RESIDUES BY A MICROSOMAL EXAMINGEN THE MACHANAL FRESIDUES BY A MICROSOMAL CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION COP PROTHROWBIN TO THROMBIN.

1- MISCELLANBOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A PROCHROMBIN E PROCHES THE ACTIVATION PEOPLES THE REMAINING PART INTO LIGHT E HEAVY CHAINS. THE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF WITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL.
FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
BY FACTOR XA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g; Glycoprotein; Repeat;
acid; Acute phase; Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTHROMBIN.
ACTIVATION PEPTIDE (FRAGMENT 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. -!- SIMILARITY: Contains 2 kringle domains.
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Vitamin K; Zymogen, Gamma-carboxyglutamic ac
Hydrolase; Serine protease; Kringle; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI 88380; F2.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001383; GLA_blood.
InterPro; IPR000001; Kringla.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PP00594; gla; 1.
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PROSITE; PS00011; GLU CARBOXYLATION PROSITE; PS00011; KRINGLE 1; 2.
PROSITE; PS50070; KRINGLE 2; 2.
PROSITE; PS50240; TRYPEIN DOM; 1.
PROSITE; PS00134; TRYPEIN HIS; 1.
PROSITE; PS00134; TRYPEIN HIS; 1.
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PRINTS; PR00001; GLABLOOD.
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PRINTS; PRO1505; PROTHROMBIN.
PRODOM; PD000395; Kringle; 2.
SMART; SM00069; GLA; 1.
SMART; SM00130; KR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X52308; CAA36548.1; -.
EMBL; M81394; AAA40435.1; -.
PIR; A35827; A35827.
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Pfam; PF00051; kringle; 2.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P00734; 1B7X.
MEROPS; S01.217; -.
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ACTIVATION PEPTIDE (FRAGMENT 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
                      THROMBIN LIGHT CHAIN (A).
THROMBIN HEAVY CHAIN (B).
KRINGLE 2.
SERINE 2.
SERINE PROTEASE.
CLEAVAGE (BY THROMBIN).
CLEAVAGE (BY TROMBIN).
CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CHARGE RELAY SYSTEM (BY SIM CARBOXYGLUTAMIC ACID GAWMA-CARBOXYGLUTAMIC ACID GAWMA-CARBOX ACID GA
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B89F719AAFD601E0 CRC64;
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553 N
70268 MW;
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618 AA;
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DISULFID
CARBOHYD
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CARBOHYD
SEQUENCE
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CHAIN
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Search completed: December 30, 2003, 09:18:42 Job time : 13 secs

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December 30, 2003, 09:16:11; Search time 34 Seconds (without alignments) 333.950 Million cell updates/sec
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1 ANSFLXXLRHGSLXRXCIXX......XXAKXIFedVDDTLAFWSKH 44
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
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sp archea:*
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sp mhc:*
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sp prodent:*
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sp virus:*
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9ttr@ canis famil	Q91wh8 mus musculu	Oggoe was mascala	Q8j002 homo sapien	Q8ixb5 homo sapien	063207 rattus norv	Q8jhc9 brachydanio	Q8n2n6 homo sapien	O54740 mus musculu	Q99132 mus musculu	O88947 mus musculu	Q96pq8 homo sapien	Q8jhc8 brachydanio	Q9gmd9 ornithorhyn	Q8jj40 xenopus lae	Ognek6 homo gapien
SUMMARIES	, QI	Q9TTR0	Q91WN8	93350	08J002	QBIXBS	963207	Овлисо	QBN2N6	054740	Q99L32	088947	Q96PQ8	QBJHCB	Q9GMD9	Q8JJ40	OBNEK6
	Query Match Length DB	456 6	460 11	460 11	55 4	55 4	482 11	443 13	231 4	481 11		481 11	701 4	474 13	469 6	229 13	268 4
مهی	Query Match L	75.0	69.5	66.5	63.0	63.0	56.5	51.2	51.0	49.5	49.5	49.5	49.0	47.5	46.5	44.0	43.5
	Score	150	139	133	126	126	113	102.5	102	66	66	66	96	95	93	88	87
	Regult No.	-	~	m	4	5	9	7	60	σ	10	11	12	13	14	15	16

P81370 hoplocephal Q15253 homo sapien Q16519 homo sapien Q9nsdo homo sapien Q91840 homo sapien	Q8t6i3 halocynthia Q28994 sus scrofa Q91001 gallus gall	Vox.30 ratura horv Q14116 homo sapien Q95nd7 pan troglod Q95nd6 pan troglod Q95n94 sus errofa	0 brachydar 1 brachydar bos taurus homo sapie	0) 7	Q8bm25 mus musculu Q8bgn6 mus musculu Q9qvh6 rattus sp. Q8tas3 homo sapien Q8x182 mus musculu Q8aye4 brachydanio Q61592 mus musculu
P83370 Q15253 Q16519 Q9NSD0 Q61109	QBT613 Q28994 Q91001	Q14316 Q15ND7 Q95ND6 Q95ND6	Q8JHD0 Q90YK1 Q95ME8 Q8IXD5	P82807 Q9PTW7 Q8IXC5 Q8CI01 Q9CQW3	Q8BM25 Q8BGN6 Q9QVH6 Q8TAS3 Q8R182 Q8RYE4
14 4 4 4 13	133	4 4 9 9	4 6 113	11.4 H	111411
376 100 650 650	542 138 607	4 4 4 4 4 4 6 6 1 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	. 44 . 44 . 44 . 44 . 45 . 45 . 45 . 45	608 241 399	226 226 179 198 503
41.5 40.0 40.0 39.5	38.8	37.5		3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	332.0 332.0 30.0 30.5 30.5
88 82 80 79	77.5	75 75 75 75	72.5 72.5 72.5	717 68 68 68	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
17 18 20 21	23 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2 2 2 2 2 3 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	38888	4 20 40 40 40 40 40 40 40 40 40 40 40 40 40	W 4 4 4 4 4 4 0 0 0 1 0 1 0 1 0 1 0 1 0 1

ALIGNMENTS

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SEQUENCE
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099PC6
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           8 ¥ 8 B
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                                                                        SMART; SMO0181; EGF; 2.

R SMART; SMO0181; EGF; 1.

R SMART; SMO0100; Tryp_SPc; 1.

R PROSITE; PS001010; Tryp_SPc; 1.

R PROSITE; PS01187; EGF=1; 1.

R PROSITE; PS01187; EGF=2; 2.

R PROSITE; PS01187; EGF=2; 1.

R PROSITE; PS01187; TRYPSIN DOM; 1.

R PROSITE; PS01185; TRYPSIN DOM; 1.

R PROSITE; PS01185; TRYPSIN SER; 1.

R EGF=11ke domain; Hydrolase; Processe; Serine protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
PROTEIN C LIGHT CHAIN.
PROTEIN C CONNECTING DIPEPTIDE.
PROTEIN C HEAVY CHAIN.
7ADJABCIC34E59FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.0%; Score 150; DB 6; Length 456; 63.6%; Pred. No. 8.8e-17; ive 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 ANSFLEEIRAGSLERECMEEICDFEEAKEIFQNVDDTLAYWSKY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL, BC013896; AAH13896.1; -.
HSSP; P00761; 1ANI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEAM, FF00089; trypain; 1.
PRINTS; PR00012; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
SWART; SM0019; EGF CA; 1.
SWART; SM00020; Tryp SPC; 1.
SWART; SM00020; Tryp SPC; 1.
PROSITE; PS001010; ASK_HYDROXYL; 1.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01181; EGF CA; 1.
PROSITE; PS01011; GLU CARBOXYLATION; 1.
PROSITE; PS00011; GLU CARBOXYLATION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:97771; Proc.
InterPro; IPR00152; Asx hydroxyl.
InterPro; IPR001814; Chymotrypsin.
InterPro; IPR001801; EGF Ca.
InterPro; IPR002509; EGF like.
InterPro; IPR002283; GLA_blood.
InterPro; IPR001284; Ser_protesse_Try.
InterPro; IPR001294; Vitk_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 194 PI
195 456 PI
456 AA; 50813 MW;
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TERMBLRel. 19, C; 01-DEC-2001 (TERMBLRel. 19, Le O1-MAR-2003 (TERMBLRel. 23, Le Similar to protein C. PROC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 63.6%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00008; EGF; 2.
Pfam; PF00594; gla; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q91WN8
Q91WN8;
                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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Q91WN8
ID 91W
AC Q91W
AC Q91W
DT 011-D
DT 011-D
DT 011-D
DT 011-D
DC C SIMI
CC C SEURA
OC NORM
OC NO
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                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                  Length 460;
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                                                                                                                                                         Query Match 69.5%; Score 139; DB 11; Length 4
Best Local Similarity 59.1%; Pred. No. 6.5e-15;
Matches 26; Conservative 7; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                        42 ANSFLEEMRPGSLERECMEEICDFEEAQEIFQNVEDTLAFWIKY 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 ANSFLEEMRPGSLERECMEEICDLEEAQEIFONVEDTLAFWIKY 85
                                                                                                                                                                                                                                                                                    1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete sequence of UC72A01.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
PROSITE; PS00134; TRYPSIN_HIS; 1. PROSITE; PS00135; TRYPSIN_ERR; 1. EGF-11Ke domain; Hydrolase; Protease; Serine protease SEQUENCE 460 AA; 51818 MW; 0117F26E68FCC274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drolase; Protease; Serine protease. 51784 MW; 0293BC25E9D3ED16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-TUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR00152; Asx hydroxyl.
InterPro; IPR00152; Asx hydroxyl.
InterPro; IPR001314; Chymctrypsin.
InterPro; IPR001381; EGF Ca.
InterPro; IPR00209; EGF Like.
InterPro; IPR00209; EGF Like.
InterPro; IPR00209; EGF Like.
InterPro; IPR00209; Yith Gep_GLA.
Pfam; PF00009; EGF; 2.
Pfam; PF00009; EGF; 2.
Pfam; PF00009; EGF; 2.
Pfam; PF00009; EGF; 1.
PRNUTS; PF00001; EGF CA; 1.
SWART; SW00010; EGF CA; 1.
SWART; SW00020; Tryp SPC; 1.
PR05ITE; PS00010; ASX_HYDROXYL; 1.
PR05ITE; PS00110; ASX_HYDROXYL; 1.
PR05ITE; PS01186; EGF Z; 2.
PR05ITE; PS01187; EGF CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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PROSITE; PS00135; TRYPSIN_SER; 1.
EGF-like domain; Hydrolase; Protea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF318182; AAK07918.1; -. HSSP; P04070; 1AUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anticoagulant protein C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGI:97771; Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            460 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=C57BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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STRAIN=Sprague-Dawley;
MEDLINE=96093366; PubMed=8578539;
Stanton C., Ross R.P., Hutson S., Wallin R.;
Stanton C., Ross R.P., Hutson S., Wallin R.;
Fordence for competition between vitamin K-dependent clotting factors for intracellular processing by the vitamin K-dependent gamma-
                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 113; DB 11; Length 482; Pred. No. 1.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.5%; Score 11., 43.2%; Pred. No. 1.7e-10; ...ive. 9; Mismatches 16; Indels ...ive. 9; Mismatches 16; Indels ...ive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 ANSFFEEIKKGNLERECVEEICSFEEAREVFEDNEKTIEFWNKY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS01180; EGF_CA; 1.
PROSITE; PS01180; EGF_CA; 1.
PROSITE; PS0011; GLU_CARBOXYLATION; 1.
PROSITE; PS00114; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN IIS; 1.
PROSITE; PS00135; TRYPSIN ER; 1.
EGF-like domain; Hydrolase; Protease; Serine protease.
SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                             Thromb. Res. 80:63-73(1995).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL. X79807; CAA56202.1; -.
HSSP; P00742; 1XXA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coagulation factor VIIi.
Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanumanthaiah R., Day K., Jagadeeswaran P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IRROUGHS; BGF_G.
InterPro; IRROUGHS; BGF_G.
InterPro; IRROUGHS; BGF_II.
InterPro; IRROUGHS; BGF_II.
InterPro; IRROUGHS; BGF_II.
InterPro; IRROUGHS; BGF_II.
InterPro; IRROUGHS; Ser_protease_Try.
InterPro; IRROUGHS; Ser_protease_Try.
InterPro; IRROUGHS; Ser_protease_Try.
InterPro; IRROUGHS; 2.
Ffam; PROUGHS; 2.
Ffam; PROUGHS; 11.
PRINTS; PROUGHS; CHYMOTRYPSIN.
PRINTS; PROUGHS; EGFBLOOD.
SMART; SMOOLS; GLABLOOD.
SMART; SMOOLS; GGA, 1.
SMART; SMOOLS; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001314; Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chymotrypsin.
EGF 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00020; Tryp SPC; 1.
ROGSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00012; EGF 1; 1.
PROSITE; PS01186; EGF 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 43.24
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S01.216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ОВЛИС9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OBJHC9
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Kinoshita S., Ilda H., Inoue S., Watanabe K., Kurihara M., Wada Y.,
Ono M., Dongchon K., Hamasaki N.;
Gene Analysis of Anticoagulation Pactors in Japanese Thrombotic
Patients. Genetic Background of Thrombophilia in Japan.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AB083700; BAC21172.1; -.

NOW TER 55 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Hamasaki S., Kang D., Kinoshita S., Iida K., Inoue S., Watanabe K.,

Kurihara M., Wada Y., Ono M.;

Korihara m., Wada Y., Ono M.;

Gene analysis of anticoagulation factors in Japanese thrombotic

patients.Genetic background of thrombophilia in Japan.";

Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, ABO86851; BAC53631.1;
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 55
55 AA; 6475 MW; 3803696534BC9289 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 AA; 6527 MW; 4F89496534A78836 CRC64;
                                                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDT 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 126; DB 4
Pred. No. 1e-13;
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                         55 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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                                                                        Created)
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                         PRT;
                                                                   01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Protein C (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 67.6%;
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.0%;
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                       PRELIMINARY;
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                               (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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es 25; Conserv
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                                                                                                                                                                                                 Homo sapiens
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SEQUENCE
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QBIXBS QBIXBS;

RESULT 5
081XB5
001XB5
AC 081XA
AC 081XB
DT 01-M
DT 01

Matches

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Gaps

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Q63207 Q63207;

RESULT 6 Q63207 ID Q632 AC Q632 DT 01-N DT 01-N

Matchea

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Heidtmann H.H., Kontermann R.E.;
"Cloning and recombinant expression of mouse coagulation factor X.";
Thromb. Res. 92:33-41(1998).
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                                                           Gaps
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Wararyota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
49.5%; Score 99; DB 11; Length 481;
Best Local Similarity 38.6%; Pred. No. 4e-08;
Matches 17; Conservative 9; Mismatches 18; Indels
  Length 231;
                                                        16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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481 COAGULATION FACTOR X.
53986 MW; CF702DE5EF9D97AE CRC64;
                                                                                                                                       20 ANEFLEELRQGTIERECMEEICSYEEVKEVFENKEKTMEFW 60
                                                                                                            1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) cognilation factor X precursor (EC 3.4.21.6).
     Query Match 51.0%; Score 102; DB 4; Best Local Similarity 41.5%; Pred. No. 5.7e-09; Matches 17; Conservative 8; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thromb. Res. 92:33-41(1998).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
EMBL; AJ222677; CAA10933.1; -.
HSSP; P00742; IXKA.
                                                                                                                                                                                                                                                                                            481 AA
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PS01186; BGF_2; 2.
PS01187; BGF_CA; 1.
PS00011; GLU_CARBOXYLATION;
                                                                                                                                                                                                                                                                                                             054740,
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR00142; EGF 2.
InterPro: IPR001481; EGF 2.
InterPro: IPR001481; EGF 7.
InterPro: IPR001481; EGF 7.
InterPro: IPR001293; EGF 7.
InterPro: IPR001294; EGF 7.
InterPro: IPR001254; Ser_Drotease Tr
InterPro: IPR001254; Ser_Drotease Tr
InterPro: IPR001254; VitK_dep_GLA.
Fam; PP00008; EGF; 2.
Pfam; PP00008; EGF; 2.
Pfam; PP00018; EGF; 2.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00011; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98454993; PubMed=9783672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000152; Asx hydroxyl InterPro; IPR001314; Chymotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0001; GLABLOOD.
SMART; SM00179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
SMART; SM00020; TrYP_SPC; 1.
PROSITE; PS00010; ASK_HYDROXYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00134; TRYPSIN_HIS; 1
PS00135; TRYPSIN_SER; 1
                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       F10 OR FA10.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; S01.216; -.
MGD; MGI:103107; F10.
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                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                 054740
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R EMBL; AKOV4574; BAC11069.1; -.
R InterPro; IPR002383; GLA blood.
R InterPro; IPR00294; Vitk_dep_GLA.
R PRINTS; PR00001; GLABLOOD.
R SMART; SM00069; GLA; 1.
R PRINTS; PR00001; GLABLOOD.
R SMART; SM00069; GLA; 1.
R PROSTIFE; PS00011; GLU CARBOXYLATION; 1.
"Comprehensive analysis of blood coagulation pathways in Teleostei:
Evolution of coagulation factor genes and identification of zebrafish
factor VIIi.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FL390093.
Hymo sapiens (Human).
Eudaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 51.2%; Score 102.5; DB 13; Length 443; 1 Similarity 47.6%; Pred. No. 9.5e-09; 20; Conservative 7; Mismatches 14; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                      1 ANS-FLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 ANSGFLEEMKAGNLERECVEEICDYEEAREVFEDDDRTKQFW 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 protein. –
231 Aa; 25844 MW; 8A373B0D5C1D0D81 CRC64;
                                                                              Blood Cells Mol. Dis. 0:0-0(2002).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL, AFF19546, AAM8342.1; -.
EMBL, AF515269, AAN71000.1; -.
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                                                                                                                                                                                InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001914; Chymotrypsin.
InterPro; IPR001981; EGF Ca.
InterPro; IPR002893; GIA blood.
InterPro; IPR002893; GIA blood.
InterPro; IPR001284; Ser protesse Try.
InterPro; IPR001254; Ser protesse Try.
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SEQUENCE 2:
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Query Match

CALTARATA A TATA A TATA

Matches

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QBNZNG

RESULT 8
008N2N6
008N2N6
01-0
01-0
01-0
01-0
02 Hypo
03 Hypo
05 Euka
06 Euka
07 Hypo
08 Hypo
09 Hypo
01 Hypo
0

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Homo sapiens (Human)
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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PROSITE;
PROSITE;
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Q96PQ8
    0.11 0.11 0.11 0.11 0.11 0.11 0.11 0.11 0.11 0.11 0.11 0.11 0.11 0.11
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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49.5%; Score 99; DB 11; Length 481;
Best Local Similarity 38.6%; Pred. No. 4e-08;
Matches 17; Conservative 9; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0723; CHYMOTRYPEIN;
PRINTS; PRO0723; CHYMOTRYPEIN.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00010; EGF_CA; 1.
SWART; SW00179; EGF_CA; 1.
SWART; SW00020; Tryp_SPC; 1.
SWART; SW00010; Tryp_SPC; 1.
PROSITE; PS001010; EGF_2; 2.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS011186; EGF_2; 2.
PROSITE; PS01011; EGF_CA; 1.
PROSITE; PS01011; EGF_CA; 1.
PROSITE; PS01013; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_ER; 1.
EGF-11ke domain; Hydrolaee; Procease; Serine protease.
SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;
41 ANSFFEEFKKGNLERECMEEICSYEEVREIFEDDEKTKEYWTKY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 ANSFFEEFKKGNLERECMEEICSYEEVREIFEDDEKTKEYWTKY 84
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ d
-1- SINILARITY: BELONGS TO PEPTIDASE FAMILY S1.
BEBL; BC003877; AAH03877.1; -.
HSSP; P00742; 1XKA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IRRO0112; Aax hydroxyl.
InterPro; IRR001114; Chymotrypsin.
InterPro; IRR001114; Chymotrypsin.
InterPro; IRR001801; EGF 2.
InterPro; IRR001838; EGF II.
InterPro; IRR001838; EGF II.
InterPro; IRR001838; EGF II.
InterPro; IRR0012383; GIA blood.
InterPro; IRR001254; Ser Protease Irv.
InterPro; IRR001254; Ser Protease Irv.
Fam; Pr00008; EGF; 2.
Fam; Pr00054; GIA: 1.
                                                                                                                                                 Created)
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                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                             Coagulation factor X
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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01-MAR-2003 (
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088947
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Gaps
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STRAIN=CSTBLE X CBA; TISSUE=Liver;
STRAIN=CSTBLE X CBA; TISSUE=Liver;
MEDLINE=98347933; PubMed=9684791;
Liang Z., Cooper A., DeFord M.E., Carmeliet P., Collen D.,
Castellino F.J., Rosen B.D.;
"Cloning and characterization of a cDNA encoding murine coagulation factor X.";
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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SIGNAL 1 40 POTENTIAL.
CARGINAT 41 481 CARGILATION FACTOR X.
SEQUENCE 481 AA, 54018 MW, 8ACO9DESEF9D271E CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cooper A., Liang Z., Castellino F.J., Rosen E.D.;
"Cloning and Characterization of the Murine Factor X Gene.";
Thromb. Haemost. 0:0-0(2000).
INILARITY: BELONGS TO PEPTIDASE FAMILY SI.
EMBL; AF087644; AAC36345.1;
EMBL; AF087644; AAC36345.1;
HSSP; D00742; IXKA.
MGD; MGI:103107; FIO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 ANSFEEFKKGNLERECMEEICSYEEVREIFEDDEKTKEYWTKY 84
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Factor VII active site mutant immunoconjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          701 AA
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PS01187; EGF_CA; 1.
PS00011; GLU_CARBOXYLATION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPRO01341; CHYMCLTYPEHIN.
InterPro; IPR001481; EGF 2.
InterPro; IPR001481; EGF 2.
InterPro; IPR001481; EGF 11.
InterPro; IPR001481; EGF 11.
InterPro; IPR001481; EGF 11.
InterPro; IPR001481; EGF 11.
InterPro; IPR001481; EGF 12.
InterPro; IPR001481; EGF 14.
InterPro; IPR001481; 1.
IPRINTS; PR00149; EGF 2.
IPRINTS; PR00101; EGFBLOOD.
IPRINTS; PR0011; EGFBLOOD.
IP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nterPro; IPR000152; Asx_hydroxylnterPro; IPR001314; Chymotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chymotrypsin.
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PSS0134; TRYPSIN HIS; 1.
PSS0135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSO0010; ASX HYDROXYL;
PROSITE; PSO0010; ASX HYDROXYL;
PROSITE; PSO0022; EGF 1: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hromb. Haemost. 80:87-91(1998)
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Best Local Similarity 38.6
Matches 17; Conservative
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SEQUENCE FROM N.A.
MEDLINE=21015017; PubMed=11132153;
Poorafshar M., Aveskogh M., Munday B., Hellman L.;
"Identification and structural analysis of four serine proteases in a monotreme, the platypus, Ornithorhynchus anatinus.";
Immunogenetics 52:19-28(2000).
Hanumanthaiah R., Day K., Jagadeeswaran P.;
"Comprehensive analysis of blood coagulation pathways in Teleostei:
Evolution of coagulation factor genes and identification of zebrafish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ornithorhynchus anatinus (Duckbill platypus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BGF-like domain, Hydrolase, Protease, Serine protease.
SEQUENCE 474 AA; 53580 MW; E1E18C1E54F27532 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.5%; Score 95; DB 13;
40.9%; Pred. No. 1.9e-07;
live 7; Mismatches 19
                                                -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
EMBL; AF275654; AAG00453.1; -.
HSSP; P00742; 1XXB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              469 AA
                                                                                                                                                          InterPro; IPR00142; GGP_G.
InterPro; IPR00143; GGF_C.
InterPro; IPR001438; EGF_C.
InterPro; IPR001438; EGF_II.
InterPro; IPR001438; GIA_blood.
InterPro; IPR001438; GIA_blood.
InterPro; IPR001454; SGF_C.
InterPro; IPR001254; SGF_D.
InterPro; IPR001254; SGF_D.
Pfam, PF00089; GGF; 2.
Pfam; PF00089; CHYMOTYPEIN.
PRINTS; PR00101; GLABLOOD.
PRINTS; PR00101; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00011; GLU CARBOXYLATION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  SWART; SW00181; EGF; 2.
SWART; SW00179; EGF CA; 1.
SWART; SW00069; GLA; 1.
SWART; SW00020; Tryp_SPC; 1.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00022; EGF 1; 1.
PROSITE; PS01166; EGF 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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InterPro; IPR001314; Chymctrypsin.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50240; TRYPSIN DOM; 1. PROSITE; PS00134; TRYPSIN HIS; 1. PROSITE; PS00135; TRYPSIN SER; 1.
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Les 18; Conservative
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Matches
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Q9GMD9
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                                                                                                                        "Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";
Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).

- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

EMBI, AF272774; AAK58686.1; --
HSSP; PO0761; IANI.
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Brachydanio rerio (Zebrafish) (Danio rerio)

Buxaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.

NCBI_TaxID=7955;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Pred. No. 9e-08;
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; TRYPSIN DOM; 1.
; TRYPSIN HIS; 1.
; TRYPSIN SER; 1.
Hydrolase; Protease; Serine protease.
A; 77826 MW; 94AC6CEB42CC992F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                       InterPro; IPR000742; EGF_2.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR001438; EGF_like.
InterPro; IPR005209; EGF_like.
InterPro; IPR0052383; Glah blood.
InterPro; IPR0071383; Glah blood.
InterPro; IPR00710; IG-like.
InterPro; IPR003597; IG_c1.
InterPro; IPR001254; SGF_Procease_Iry.
InterPro; IPR001254; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF_CA; 1.
GLU_CARBOXYLATION; 1.
                                                                     SEQUENCE FROM N.A. MEDLINE=21477448; Pubmed=11593034;
                                                                                                                                                                                                                                     InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000742; EGF 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00407; IGC1; 1.
-SMART; SM00202; TYP, SPC; 1.
PROSITE; PS00010; ASK HYDROXYL;
PROSITE; PS00022; EGF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PF00089; trypsin, 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00010; EGFBLOOD.
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Bust Local Similarity 48.00,

Bust Local Similarity 48.00,
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SMART; SM00179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
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SEQUENCE FROM N.A.
                                                                                                           Hu Z., Garen A.;
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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DR PRINTS; PR0012; CHYMOTRYPSIN.

DR SWART; SM00179; EGF CA; 1.

SWART; SM00020; TryPs SPC; 1.

RMART; SM00020; TryPs SPC; 1.

PROSITE; PS00010; GLAF DOM; 1.

PROSITE; PS01186; EGF 1; 1.

"QSITE; PS01186; EGF 2; 2.

"STE; PS01186; EGF 2; 2.

"STE; PS01187; EGF CA; 1.

"TE; PS01187; EGF CA; 1.

"AS SCOUTH; TRYPSIN HIS; 1.

"S00135; TRYPSIN HIS; 1.

"S00135; TRYPSIN HIS; 1.

"AA; 52196 MW; 4C66C230D0758F6A CRC64; 40.54; Pred. No. 4.18-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 14-07; 
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MEDLINE-21676254; PubMed=11818060;
Georgi A.B., Stukenberg P.T., Kirschner M.W.;
Tiffing of events in mitosis.";
Curr. Biol. 12:105-114(2002).
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01-0CT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last and
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Xenopus laevis (African clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches 15; Conservative
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US-08-484-568-2
US-08-774-592-2
US-08-487-037-2
US-08-487-037-3
US-08-469-658-53
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ORGANISM: Homo sapiens
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Sequence 24, Appl
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Sequence 5, Appli
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                                                                          December 30, 2003, 09:17:31 ; Search time 21 Seconds (without alignments) 88.651 Million cell updates/sec
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                                                                                                                                                1 ANSFLXXLRHGSLXRXCIXX.....xxAKXIFedVDDTLAFWSKH
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(c) 1993 - 2003 Compugen Ltd.
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OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
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Sequence 19, Application US/08955636A
Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: POLYMEPTIDES
TITLE OF INVENTION: POLYMEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE FRACESEQ for Windows Version 3.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-08-955-636-24

i Sequence 24, Application US/08955636A

i Patent No. 6017882

i GENERAL INFORMATION:
    APPLICANT: Nelsestuen, Gary

ITILE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT:
    TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 09531/002001

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT APPLICATION NUMBER: US/08/955,636A

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 24
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
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CTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid US-08-955-636-24
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                                                                                                          Query Match 87.0%; Score 174; DB 3; Length 44; Best Local Similarity 97.7%; Pred. No. 3.5e-22; Matches 43; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      FACEUR NO. 9017081.

APPLICANT: Nelsestuen, Gary
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MOIFFED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYBEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT PILION DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 35
LENGTH: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
ITILE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT;
ITILE OF INVENTION: POLYPEPTIDES
ITILE OF INVENTION: POLYPEPTIDES;
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                ; Sequence 35; Application US/08955636A; Patent No. 6017882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/08955636A
; Patent No. 6017882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MOD RES
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US-08-955-636-35
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US-08-955-636-1
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Gaps
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1 LOCATION: (0)...(0).

2 CTHER INFORMATION: Xaa-gamma carboxyglutamic acid or glutamic acid

US-08-955-636-20
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84.0%; Score 168; DB 3; Length 44

Best Local Similarity 95.5%; Pred. No. 3.5e-21;

Matches 42; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 95.5%; Pred. No. 3.5e-21;
Matches 42; Conservative 0; Mismatches 2; Indels
1 ANSFLXXLRHSSLXRXCIXXICDFXXARCXIFQNVDDTLAFWSKH 44
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                                                                                                                                       Sequence 20, Application US/08955636A

Sequence 20, Application US/08955636A

Patent No. 6017882

GENERAL INFORMATION:

APPLICANT: Nelsestuen, Gary

TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT

TITLE OF INVENTION: POLYPEPTIDES

FILE REFERENCE: 09531/002001

CURRENT PILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PastSEQ for Windows Version 3.0

SEQ ID NO 30

LENGTH: 44
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Fatent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/00201
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 21
LENGTH: 44
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US-08-955-636-25
Sequence 25, Application US/08955636A
Patent No. 6017882
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TYPE: amino acid
TOPOLOGY: linear
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ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 92037
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. OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid US-08-955-636-25
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84.0%; Score 168; DB 3; Length 44;
Best Local Similarity 95.5%; Pred. No. 3.5e-21;
Matches 42; Conservative 0; Mismatches 2; Indels
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ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTEN RE-BOS/MS-DOS
SOFTWARE: PARENTEN RO-BOS/MS-DOS
SOFTWARE: PARENTEN RO-BOS/MS-DOS
SOFTWARE: PARENTEN RO-BOS/MS-DOS
SOFTWARE: PARENTEN RO-BOS/MS-DOS
FLING DATE: 7-NOV-1997
CLASSITCATION NUMBER: US/08/965,832
FLING DATE: 8-NOV-1997
APPLICATION NUMBER: 08/745,254
FLING DATE: 8-NOV-1996
PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/053,768
FLING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: PADEC, PATERA L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 165/167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08965832
Patent No. 5847085
GENERAL INFORMATION:
TAPLICANT: CHARLES T. ESMON AND MIKHAIL D. SMIRNOV TITLE OF INVENTION: Modified Protein C
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West
APPLICANT: Nolsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
FITLE OF INVENTION: POLYEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT PILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FABELSEQ for Windows Version 3.0
SEQ ID NO 25
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TELEPAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Atlanta
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US-08-965-832-2
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GENERAL INFORMATION:

APPLICANT: Griffin, John H.

APPLICANT: Graters, Rolf M.

APPLICANT: Mesters, Rolf M.

TITLE OF INVENTION: Serine Protease-Derived Polypeptides and

TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods

TITLE OF INVENTION: for Inhibiting Coagulation

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                          . LOCATION:
; OTHER INFORMATION: /note= "partial sequence of human protein C"
US-08-965-832-2
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0
                                                                                                                                                                                                                                                                              Length 45
                                                                                                                                                                                                                                                                            Query Match 84.0%; Score 168; DB 2; Length 45
Best Local Similarity 93.2%; Pred. No. 3.6e-21;
Matches 41; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFQNVDDTLAFWSKH 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Office of Patent Counsel, The Scripps ADDRESSEE: Research Institute STREET: 10666 No. 5679639th Torrey Pines Road, TPC CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OSPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION 530
PRIOR APPLICATION TOWBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION NUMBER: 34,163
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: TSRISG3.0C1
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1.157
OTHER INFORMATION: /note= "Protein C Light Chain"
FEATURE:
NAME/KEY:

LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29
COTHER INFORMATION: /note= "where Kaa means gamma OTHER INFORMATION: carboxylglutamic acid"
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08295411
Patent No. 5679639
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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OTHER INFORMATION: Peptide"
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                                                                 LOCATION: 170..419
; OTHER INFORMATION:
US-08-955-471-1
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TYPE: PRT
ORGANISM: Homo sapiens
             PEATURE:
NAME/KEY: Region
170..4
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08955471
Patent No. 5968751
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF SEQUENCES: 10
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                              ö
                                                                                                                                                                                               84.0%; Score 168; DB 1; Length 419; llarity 72.7%; Pred. No. 4.4e-20; Conservative 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                               1 ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                    1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Region
LOCATION: 1..157
OTHER INFORMATION: /note= "Protein C Light Chain"
                                                                                                         LOCATION: 170..419
COTHER INFORMATION: /note= "Protein C Heavy Chain"
US-08-295-411-1
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LOCATION: 158..169
OTHER INFORMATION: /note= "Protein C Activation
                        /note= "Protein C Activation
Peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFRENCE/POCKET NUMBER: TSRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 419 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
LOCATION: 158.,169
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                     NAME/KEY: Region
                                                                                                                                                                                                                     Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 92037
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US-08-955-471-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                   Query Match
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APPLICANT: Griffin, John H.
APPLICANT: Mesters. Rolf
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SURCESS:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Baker, Jeffrey C
APPLICANT: Carlson, Andrew D
APPLICANT: Carlson, Andrew D
APPLICANT: Huang, Lihua
APPLICANT: Huang, Lihua
APPLICANT: Sheliga, Throdore A
TITLE OF INVENTION: Improved Methods for Processing Activated Protein C
FILE REFERENCE: X-11796A
CURRENT APPLICATION NUMBER: US/09/667,570A
CURRENT APPLICATION NUMBER: 60/045,255
PRIOR PLILING DATE: 1997-04-28
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                                                                              Length 419;
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                                                                              Score 168; DB 2; Length 41
Pred. No. 4.4e-20;
2; Mismatches 10; Indels
                                                                                                                                                                                                                       1 ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDTLAFWSKH 44
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/note= "Protein C Heavy Chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 10666 North Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 168; DB 4;
Pred. No. 4.4e-20;
2; Mismatches 10
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
                                                                              Query Match
Best Local Similarity 72.7%;
Matches 32; Conservative
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Best Local Similarity 72.7%;
Matches 32; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-756-506-2
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 32; Conserva
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Pred. No. 4.4e-20;
2; Mismatches 10; Indels
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APPLICANT: Cottingham, Ian R.
APPLICANT: Temperley, Simon M.
APPLICANT: Foster, Donald C.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Donna E.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Protein C Light Chain"
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Peptide"
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COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
                          PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-00V-1991
ATTOCNEV, AGGNT INFORMATION:
NAME: Fitting, Thomas
REGISTATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR0472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-54-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                            TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 84.0%;
1 Similarity 72.7%;
32; Conservative ;
19921118
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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COMPUTER READABLE FORM:
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ADDRESSEE: ZymoGenet
STREET: 1201 Eastlak
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LOCATION: 158..169
OTHER INFORMATION: /
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CCATION: 170..419
CTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
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Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Spreeher, Cindy A.
APPLICANT: Prunkard, Donna E.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: ANIMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
                                                                                                                                                                                                                                                                     Score 168; DB:
Pred. No. 4.9e-:
2; Mismatches
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Pred. No. 4
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08756506
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TELECOMMUNICATION INFORMATION
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                     84.0%;
milarity 72.7%;
Conservative 2
                               REFERENCE/DOCKET NUMBER: 9
TELECOMMUNICATION INFORMATION
TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 72.7%;
Matches 32; Conservative
                                                                                   TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 460 amino acids TYPE: amino acids TYPE: amino acids TOPOLOGY: linear
Deborah A
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amino acid
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Search completed: December 30, 2003, 09:20:38 Job time: 22 secs

1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

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US-10-168-407-4
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282.476 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
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| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp:*
| cgn2_6/ptodata/2/pubpaa/USO08_PUBCOMB.ppp:*
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                                                                                                                                                                                                December 30, 2003, 09:19:36 ; Search time 31 Seconds
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-10-168-407-4
US-10-182-263-3
US-10-182-263-5
US-10-182-263-5
US-10-168-407-5
US-10-168-407-6
US-10-182-263-6
US-10-182-263-6
US-10-182-263-1
US-09-978-917A-4
US-10-168-407-1
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US-10-168-407-1
US-00-168-407-1
US-00-168-203-1
US-01-168-203-1
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US-10-168-203-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0 Maximum DB seq length: 20000000000
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Match Length DB
                               Copyright
                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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Sequence 18,
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US-10-248-504-44
US-10-298-330-18
US-09-782-587B-3
US-10-375-741-14
US-10-298-330-3
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US-10-188-495-41
US-10-188-495-42
US-10-189-123-43
US-10-189-123-43
US-10-189-123-43
US-10-189-123-43
US-10-189-123-40
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ALIGNMENTS

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US-10-168-407-3

US-10-168-407-3

Publication No. US20030207435A1

GENERAL INFORMATION:
GENERAL INFORMATION:
FOURTHORN BROYEN C DERIVATIVES

TITLE OF INFORMATION:
CURRENT FILING DATE:
CURRENT FILING DATE:
CURRENT FILING DATE:
CURRENT FILING DATE:
SOFTWARE:
PAPELICANION NUMBER: US/10/168,407

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Gaps

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Length 419;

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1 ANSFLEELRHGSLERECIEBICDFEBAKEIFEDVDDTLAFWSKH 44
                                                                                                                  1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                       Query Match
91.0%; Score 182; DB 15;
Best Local Similarity 79.5%; Pred. No. 3.2e-22;
Matches 35; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                    APPLICANT: Gerlitz, Bruce E
APPLICANT: Gerlitz, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/189199
PRIOR PILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 5:
SEQ ID NO 5:
                                                                                                                                                                                                                               US-10-182-263-5
; Sequence 5. Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
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Best Local Similarity 79.5%;
Matches 35; Conservative
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Best Local Similarity 77.3%;
Matches 34; Conservative
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ORGANISM: Homo sapiens
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   US-10-182-263-4
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Pred. No. 3.2e-22;
0; Mismatches 9; Indels
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Fublication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian E
APPLICANT: Grinnell, Brian E
APPLICANT: Grinnell, Brian E
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT APPLICATION NUMBER: US/10/182,263
PRIOR APPLICATION NUMBER: 60/181948
PRIOR PILING DATE: 2002-02-11
PRIOR FILING DATE: 2002-01-14
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 419
TYPE: PRT
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Best Local Similarity 79.5%;
Matches 35; Conservative (
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SCTWARE: Patentin version 3.1
SEQ ID NO 3
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US-10-168-407-4
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ORGANISM: Homo sapiens
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Length 419;
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Score 182; DB 15;
Pred. No. 3.2e-22;
0; Mismatches 9;
                                                                                                                                                                                                                        ; Sequence 5. Application US/10168407
; Publication No. US20030207435A1
; GENERAL INFORMATION:
   APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13610
; CURRENT APPLICATION NUMBER: US/10/168,407
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5.2
; LENGTH: 419
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Gaps

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FEATURE:

NAME/KEY: VARIANT

LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29

CTHER INFORMATION: Xaa = gamma carboxyglutamic or glutamic acid
US-10-298-330-1
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Pred. No. 7.3e-20;
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84.0%; Score 168; DB 15;
Best Local Similarity 93.2%; Pred. No. 6.1e-21;
Matches 41; Conservative 2; Mismatches 1;
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Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: GRAILIZ, Bruce E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SEOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 419
PRIOR APPLICATION NUMBER: 09/302,239
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 08/955,636
PRIOR FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
SEQ ID NO 1
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Sequence 1, Application US/10298330

Publication No. US20030100506A1

GENERAL INFORMATION:

TITLE OF INVENTION: Modified Vitamin K-Dependent

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 09531-127001

CURRENT APPLICATION NUMBER: US/10/298,330

CURRENT FILING DATE: 2002-11-18

PRIOR PELICATION NUMBER: 09/497,591

PRIOR FILING DATE: 2000-02-03
                Sequence 6, Application US/10168407
Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
ITLE OP INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 6
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APPLICANT: Gones, Bryan E
APPLICANT: Gones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: 05/181948
FILING DATE: 2002-07-22
PRIOR FILING DATE: 2002-07-11
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VETSION 3.1
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TYPE: PRT
CRGANISM: Homo sapiens
US-10-168-407-6
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LENGTH: 419
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US-10-182-263-6
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1 ANSFLXXLRHGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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Pred. No. 8.1e-20;
2; Mismatches 10;
                               Sequence 2, Application US/10168407
Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REPERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 2
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Best Local Similarity 72.7%;
Matches 32; Conservative
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Best Local Similarity 72.7°
Matches 32; Conservative
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ORGANISM: Homo sapiens
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US-10-182-263-2
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Publication No. US20030027299A1
GENERAL INFORMATION:
APPLICANT MAXYGEN Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219us110 - protein C
CURRENT APPLICATION NUMBER: US/09/978,917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2.
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Pred. No. 8.1e-20;
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10; Indels
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Pred. No. 7.3e-20;
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Mismatches
                                                                                                                                                                                                                                                            APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REPERRICE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR FILING DATE: 2002-07-11
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 1
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Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
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Best Local Similarity 72.73
Matches 32; Conservative
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32; Conservative
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US-10-182-263-1
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US-09-978-917A-2
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Best Local Similarity
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US-09-978-917A-2
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43 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKH 86
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Pred. No. 8.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                       APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR PELING DATE: 2002-02-11
PRIOR FILING DATE: 2000-03-14
PRIOR PILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 2
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Job time : 32 secs
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